

# SEQUENCE LISTING

<110> Andre R. Abad  
 Nicholas B. Duck  
 Xiang Feng  
 Ronald D. Flannagan  
 Theodore W. Kahn  
 Lynn E. Sims

<120> Genes Encoding Novel Proteins With  
 Pesticidal Activity Against Coleopterans

<130> 35718/237005

<150> 60/242,838

<151> 2000-10-24

<160> 48

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3621

<212> DNA

<213> *Bacillus thuringiensis*

<220>

<221> CDS

<222> (1)...(3621)

<221> misc\_feature

<222> (0)...(0)

<223> Cry1218-1

<400> 1

atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct	48
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	

100	105	110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca			384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala			
115	120	125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat			432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn			
130	135	140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca			480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro			
145	150	155	160
aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt gaa atc ctg			528
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu			
165	170	175	
gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca aat ttt			576
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe			
180	185	190	
gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt cat tta			624
Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu			
195	200	205	
ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga tgg tca			672
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser			
210	215	220	
aca act act att aat aac tat tat gat cgt caa atg aaa ctt act gca			720
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala			
225	230	235	240
gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca aaa			768
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys			
245	250	255	
tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa ttc cgt			816
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg			
260	265	270	
aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc cca aat			864
Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn			
275	280	285	
tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca agg			912
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg			
290	295	300	
gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca att ggt			960
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly			
305	310	315	320
tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca tcc gtt			1008
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val			
325	330	335	
att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg tat			1056
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr			
340	345	350	
aca caa tca aga agc att tct tcc gct cgc tat ata aga cat tgg gct			1104

Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	Ala		
	355						360					365					
ggt	cat	caa	ata	agc	tac	cat	cgt	gtc	agt	agg	ggt	agt	aat	ctt	caa	1152	
Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	Ser	Asn	Leu	Gln		
	370					375					380						
caa	atg	tat	gga	act	aat	caa	aat	cta	cac	agc	act	agt	acc	ttt	gat	1200	
Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	Phe	Asp		
	385				390					395					400		
ttt	acg	aat	tat	gat	att	tac	aag	act	cta	tca	aag	gat	gca	gta	ctc	1248	
Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu		
			405						410					415			
ctt	gat	att	gtt	tac	cct	ggg	tat	acg	tat	ata	ttt	ttt	gga	atg	cca	1296	
Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	Pro		
			420					425					430				
gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	aat	aat	acc	aga	aag	acg	1344	
Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	Thr		
		435					440					445					
tta	aag	tat	aat	cca	gtt	tcc	aaa	gat	att	ata	gcg	agt	aca	aga	gat	1392	
Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	Ser	Thr	Arg	Asp		
	450					455					460						
tcg	gaa	tta	gaa	tta	cct	cca	gaa	act	tca	gat	caa	cca	aat	tat	gag	1440	
Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln	Pro	Asn	Tyr	Glu		
	465				470					475					480		
tca	tat	agc	cat	aga	tta	tgt	cat	atc	aca	agt	att	ccc	gcg	acg	ggg	1488	
Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	Pro	Ala	Thr	Gly		
				485				490						495			
aac	act	acc	gga	tta	gta	cct	gta	ttt	tct	tgg	aca	cat	cga	agt	gca	1536	
Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala		
			500					505					510				
gat	tta	aac	aat	aca	ata	tat	tca	gat	aaa	atc	act	caa	att	ccg	gcc	1584	
Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	Gln	Ile	Pro	Ala		
		515					520					525					
gtt	aaa	tgt	tgg	gat	aat	tta	ccg	ttt	gtt	cca	gtg	gta	aaa	gga	cca	1632	
Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val	Val	Lys	Gly	Pro		
	530					535					540						
gga	cat	aca	gga	ggg	gat	tta	tta	cag	tat	aat	aga	agt	act	ggg	tct	1680	
Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg	Ser	Thr	Gly	Ser		
	545				550				555					560			
gta	gga	acc	tta	ttt	cta	gct	cga	tat	ggc	cta	gca	tta	gaa	aaa	gca	1728	
Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala	Leu	Glu	Lys	Ala		
				565				570					575				
ggg	aaa	tat	cgt	gta	aga	ctg	aga	tat	gct	act	gat	gca	gat	att	gta	1776	
Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp	Ala	Asp	Ile	Val		
			580					585					590				
ttg	cat	gta	aac	gat	gct	cag	att	cag	atg	cca	aaa	aca	atg	aac	cca	1824	
Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys	Thr	Met	Asn	Pro		
		595					600					605					

ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc aca Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr 610 615 620	1872
aca tta aat tta gca aca gat agt tgc cta gca ttg aaa cat aat tta Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu 625 630 635 640	1920
ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac cga Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg 645 650 655	1968
atc gaa ttc atc cca gta gat gag aca tat gaa gcg gaa caa gat tta Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu Gln Asp Leu 660 665 670	2016
gaa gca gcg aag aaa gca gtg aat gcc ttg ttt acg aat aca aaa gat Glu Ala Ala Lys Lys Ala Val Asn Ala Leu Phe Thr Asn Thr Lys Asp 675 680 685	2064
ggc tta cga cca ggc gta acg gat tat gaa gtg aat caa gcg gca aac Gly Leu Arg Pro Gly Val Thr Asp Tyr Glu Val Asn Gln Ala Ala Asn 690 695 700	2112
tta gtg gaa tgc cta tgc gat gat ttg tat cca aat gaa aaa cga ttg Leu Val Glu Cys Leu Ser Asp Asp Leu Tyr Pro Asn Glu Lys Arg Leu 705 710 715 720	2160
tta ttt gat gca gtg aga gag gca aaa cgc ctc agt gag gca cgt aat Leu Phe Asp Ala Val Arg Glu Ala Lys Arg Leu Ser Glu Ala Arg Asn 725 730 735	2208
ttg ctt caa gat cca gat ttc caa gag ata aat gga gaa aat ggc tgg Leu Leu Gln Asp Pro Asp Phe Gln Glu Ile Asn Gly Glu Asn Gly Trp 740 745 750	2256
acg gca agt acg gga att gag gtt ata gaa ggg gat gct tta ttc aaa Thr Ala Ser Thr Gly Ile Glu Val Ile Glu Gly Asp Ala Leu Phe Lys 755 760 765	2304
ggg cgt tat cta cgc cta cca ggt gcg aga gaa ata gat acg gaa acg Gly Arg Tyr Leu Arg Leu Pro Gly Ala Arg Glu Ile Asp Thr Glu Thr 770 775 780	2352
tat cca acg tat ctg tat caa aaa gta gag gaa ggt gta tta aaa cca Tyr Pro Thr Tyr Leu Tyr Gln Lys Val Glu Glu Gly Val Leu Lys Pro 785 790 795 800	2400
tac aca aga tat aga ttg aga ggg ttt gtc gga agc agt caa gga ttg Tyr Thr Arg Tyr Arg Leu Arg Gly Phe Val Gly Ser Ser Gln Gly Leu 805 810 815	2448
gaa att ttc aca att cgt cat caa acg aac cga att gta aaa aat gta Glu Ile Phe Thr Ile Arg His Gln Thr Asn Arg Ile Val Lys Asn Val 820 825 830	2496
ccg gat gat ttg ctg cca gat gta tct cct gtt aac tgc gat ggt agt Pro Asp Asp Leu Leu Pro Asp Val Ser Pro Val Asn Ser Asp Gly Ser 835 840 845	2544
atc aat cga tgc agc gaa caa aag tat gtg aat agc cgt tta gaa gta Ile Asn Arg Cys Ser Glu Gln Lys Tyr Val Asn Ser Arg Leu Glu Val 850 855 860	2592



gaa aac cgt tct ggt gaa gcg cat gag ttc tct att cct att gat aca	2640
Glu Asn Arg Ser Gly Glu Ala His Glu Phe Ser Ile Pro Ile Asp Thr	
865 870 875 880	
ggt gaa atc gat tac aat gaa aat gca gga ata tgg gtt gga ttt aag	2688
Gly Glu Ile Asp Tyr Asn Glu Asn Ala Gly Ile Trp Val Gly Phe Lys	
885 890 895	
att acg gac cca gag gga tat gca aca ctc gga aac cta gaa ttg gtc	2736
Ile Thr Asp Pro Glu Gly Tyr Ala Thr Leu Gly Asn Leu Glu Leu Val	
900 905 910	
gaa gag gga cct tta tca gga gac gca tta gaa cgc ttg caa aga gaa	2784
Glu Glu Gly Pro Leu Ser Gly Asp Ala Leu Glu Arg Leu Gln Arg Glu	
915 920 925	
gaa caa cag tgg aag att caa atg aca aga aga cgt gaa gaa aca gat	2832
Glu Gln Gln Trp Lys Ile Gln Met Thr Arg Arg Arg Glu Glu Thr Asp	
930 935 940	
aga agg tat atg gca tcg aaa caa gcg gta gat cgt tta tat gcc gat	2880
Arg Arg Tyr Met Ala Ser Lys Gln Ala Val Asp Arg Leu Tyr Ala Asp	
945 950 955 960	
tat cag gat cag caa ctg aat cct gat gta gag att aca gat ctt act	2928
Tyr Gln Asp Gln Gln Leu Asn Pro Asp Val Glu Ile Thr Asp Leu Thr	
965 970 975	
gcg gcc caa gat ctg ata cag tcc att cct tac gta tat aac gaa atg	2976
Ala Ala Gln Asp Leu Ile Gln Ser Ile Pro Tyr Val Tyr Asn Glu Met	
980 985 990	
ttc cca gaa ata cca ggg atg aac tat acg aag ttt aca gaa tta aca	3024
Phe Pro Glu Ile Pro Gly Met Asn Tyr Thr Lys Phe Thr Glu Leu Thr	
995 1000 1005	
gat cga ctc caa caa gcg tgg agt ttg tat gat cag cga aat gcc ata	3072
Asp Arg Leu Gln Gln Ala Trp Ser Leu Tyr Asp Gln Arg Asn Ala Ile	
1010 1015 1020	
cca aat ggt gat ttt cga aat ggg tta agt aat tgg aat gca acg cct	3120
Pro Asn Gly Asp Phe Arg Asn Gly Leu Ser Asn Trp Asn Ala Thr Pro	
1025 1030 1035 1040	
ggc gta gaa gta caa caa atc aat cat aca tct gtc ctt gtg att cca	3168
Gly Val Glu Val Gln Gln Ile Asn His Thr Ser Val Leu Val Ile Pro	
1045 1050 1055	
aac tgg gat gag caa gtt tcg caa cag ttt aca gtt caa ccg aat caa	3216
Asn Trp Asp Glu Gln Val Ser Gln Gln Phe Thr Val Gln Pro Asn Gln	
1060 1065 1070	
aga tat gtg tta cga gtt act gcg aga aaa gaa ggg gta gga aat gga	3264
Arg Tyr Val Leu Arg Val Thr Ala Arg Lys Glu Gly Val Gly Asn Gly	
1075 1080 1085	
tat gta agt atc cgt gat ggt gga aat caa aca gaa acg ctt act ttt	3312
Tyr Val Ser Ile Arg Asp Gly Gly Asn Gln Thr Glu Thr Leu Thr Phe	
1090 1095 1100	
agt gca agc gat tat gat aca aat gga atg tat aat acg caa gtg tcc	3360
Ser Ala Ser Asp Tyr Asp Thr Asn Gly Met Tyr Asn Thr Gln Val Ser	

1105	1110	1115	1120	
aat aca aat gga tat aac aca aat aat gcg tat aat aca caa gca tcg				3408
Asn Thr Asn Gly Tyr Asn Thr Asn Asn Ala Tyr Asn Thr Gln Ala Ser				
1125	1130	1135		
agt aca aac gga tat aac gca aat aat atg tat aat acg caa gca tcg				3456
Ser Thr Asn Gly Tyr Asn Ala Asn Asn Met Tyr Asn Thr Gln Ala Ser				
1140	1145	1150		
aat aca aac gga tat aac aca aat agt gtg tac aat gat caa acc ggc				3504
Asn Thr Asn Gly Tyr Asn Thr Asn Ser Val Tyr Asn Asp Gln Thr Gly				
1155	1160	1165		
tat atc aca aaa aca gtg aca ttc atc ccg tat aca gat caa atg tgg				3552
Tyr Ile Thr Lys Thr Val Thr Phe Ile Pro Tyr Thr Asp Gln Met Trp				
1170	1175	1180		
att gag atg agt gag aca gaa ggt aca ttc tat ata gaa agt gta gaa				3600
Ile Glu Met Ser Glu Thr Glu Gly Thr Phe Tyr Ile Glu Ser Val Glu				
1185	1190	1195	1200	
ttg att gta gac gta gag taa				3621
Leu Ile Val Asp Val Glu *				
1205				

<210> 2  
 <211> 1206  
 <212> PRT  
 <213> *Bacillus thuringiensis*

<400> 2

Met	Ser	Pro	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Thr	Pro
1				5					10					15	
Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu
			20					25					30		
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met
		35				40					45				
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val
	50					55					60				
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu
65					70				75						80
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr
			85						90					95	
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp
		100						105					110		
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala
	115						120					125			
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn
	130					135					140				
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro
145					150					155					160
Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg	Phe	Glu	Ile	Leu
			165						170					175	
Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg	Val	Thr	Asn	Phe
		180						185					190		
Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	Asn	Leu	His	Leu
		195					200					205			
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	Trp	Ser
	210					215					220				
Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	Ala
225					230					235					240

Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys  
 245 250 255  
 Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg  
 260 265 270  
 Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn  
 275 280 285  
 Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg  
 290 295 300  
 Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly  
 305 310 315 320  
 Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val  
 325 330 335  
 Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr  
 340 345 350  
 Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala  
 355 360 365  
 Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln  
 370 375 380  
 Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp  
 385 390 395 400  
 Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu  
 405 410 415  
 Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro  
 420 425 430  
 Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr  
 435 440 445  
 Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp  
 450 455 460  
 Ser Glu Leu Glu Leu Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu  
 465 470 475 480  
 Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly  
 485 490 495  
 Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala  
 500 505 510  
 Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala  
 515 520 525  
 Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Lys Gly Pro  
 530 535 540  
 Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser  
 545 550 555 560  
 Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala  
 565 570 575  
 Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val  
 580 585 590  
 Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro  
 595 600 605  
 Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr  
 610 615 620  
 Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu  
 625 630 635 640  
 Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg  
 645 650 655  
 Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu Gln Asp Leu  
 660 665 670  
 Glu Ala Ala Lys Lys Ala Val Asn Ala Leu Phe Thr Asn Thr Lys Asp  
 675 680 685  
 Gly Leu Arg Pro Gly Val Thr Asp Tyr Glu Val Asn Gln Ala Ala Asn  
 690 695 700  
 Leu Val Glu Cys Leu Ser Asp Asp Leu Tyr Pro Asn Glu Lys Arg Leu  
 705 710 715 720  
 Leu Phe Asp Ala Val Arg Glu Ala Lys Arg Leu Ser Glu Ala Arg Asn  
 725 730 735  
 Leu Leu Gln Asp Pro Asp Phe Gln Glu Ile Asn Gly Glu Asn Gly Trp



<212> DNA  
 <213> Bacillus thuringiensis

<220>  
 <221> CDS  
 <222> (1)...(3633)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> Cry1218-2

```

<400> 3
atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95

act caa ctt att gat att ctg tgg cct tca ggg caa aag agt caa tgg 336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp
100 105 110

gag att ttt atg gaa caa gta gaa gaa ctc ata aat caa aaa ata gca 384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg aaa gaa aat cca 480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro
145 150 155 160

aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt gaa atc ctg 528
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
165 170 175

gat agt tta ttt acg caa tac atg cca tct ttt cga gtg aca aat ttt 576
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
180 185 190

gaa gta cca ttc ctt aca gta tat aca cag gca gcc aac ctt cat tta 624
Glu Val Pro Phe Leu Thr Val Thr Thr Gln Ala Ala Asn Leu His Leu
195 200 205

```

ctg tta tta aag gac gct tca att ttt gga gaa gaa tgg gga tgg tct	672
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser	
210 215 220	
aca acc act att aat aac tat tat gat cgt caa atg aaa ctt act gca	720
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala	
225 230 235 240	
gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca aaa	768
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys	
245 250 255	
tta aaa ggc acg agc gct aaa caa tgg gtc gac tat aac caa ttc cgt	816
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg	
260 265 270	
aga gaa atg aca ctg acg gtt tta gat gtt gtt gca tta ttc cca aat	864
Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn	
275 280 285	
tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca agg	912
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg	
290 295 300	
gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca att ggt	960
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly	
305 310 315 320	
tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca tcc gtt	1008
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val	
325 330 335	
att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg tat	1056
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr	
340 345 350	
aca caa tca aga agc att tct tcc gct cgc tat ata aga cat tgg gct	1104
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala	
355 360 365	
ggc cat caa ata agc tat cat cgg att ttt agt gat aat att ata aaa	1152
Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys	
370 375 380	
cag atg tat gga act aat caa aat cta cac agc act agt acc ttt gat	1200
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp	
385 390 395 400	
ttt acg aat tat gat att tac aag acg tta tca aaa gat gcg gtg ctc	1248
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu	
405 410 415	
ctt gat att gtt ttt cct ggt tat acg tat ata ttt ttt gga atg cca	1296
Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro	
420 425 430	
gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga aag acg	1344
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr	
435 440 445	
tta aag tat aat ccg gtt tcc aaa gat att ata gcg ggg aca aga gat	1392
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Gly Thr Arg Asp	

450	455	460	
tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat tat gag			1440
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu			
465	470	475	480
tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg ggt			1488
Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly			
	485	490	495
tca act acc gga tta gta cct gta ttt tct tgg aca cat cgg agt gcc			1536
Ser Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala			
	500	505	510
gat ctt ata aat gca gtt cat tca gat aaa att act cag att ccg gtc			1584
Asp Leu Ile Asn Ala Val His Ser Asp Lys Ile Thr Gln Ile Pro Val			
	515	520	525
gta aag gtt tct gat ttg gct ccc tct ata aca gga ggg cca aat aat			1632
Val Lys Val Ser Asp Leu Ala Pro Ser Ile Thr Gly Gly Pro Asn Asn			
	530	535	540
acc gtt gta tcg ggt cct gga ttt aca ggg ggg ggg ata ata aaa gta			1680
Thr Val Val Ser Gly Pro Gly Phe Thr Gly Gly Ile Ile Lys Val			
	545	550	555
ata aga aat gga gta att ata tca cat atg cgt gtt aaa att tca gac			1728
Ile Arg Asn Gly Val Ile Ile Ser His Met Arg Val Lys Ile Ser Asp			
	565	570	575
att aac aaa gaa tat agt atg agg att cgg tat gct tcc gct aat aat			1776
Ile Asn Lys Glu Tyr Ser Met Arg Ile Arg Tyr Ala Ser Ala Asn Asn			
	580	585	590
act gaa ttt tat ata aat cct tct gaa gaa aac gtt aaa tct cac gct			1824
Thr Glu Phe Tyr Ile Asn Pro Ser Glu Glu Asn Val Lys Ser His Ala			
	595	600	605
caa aaa act atg aat aga ggt gaa gct tta aca tat aat aaa ttt aat			1872
Gln Lys Thr Met Asn Arg Gly Glu Ala Leu Thr Tyr Asn Lys Phe Asn			
	610	615	620
tat gcg act ttg ccc cct att aaa ttt acg aca acc gaa cct ttc att			1920
Tyr Ala Thr Leu Pro Pro Ile Lys Phe Thr Thr Thr Glu Pro Phe Ile			
	625	630	635
act cta ggg gct ata ttt gaa gcg gaa gac ttt ctt gga att gaa gct			1968
Thr Leu Gly Ala Ile Phe Glu Ala Glu Asp Phe Leu Gly Ile Glu Ala			
	645	650	655
tat ata gac cga atc gaa ttt atc cca gta gat gag aca tat gaa gcg			2016
Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala			
	660	665	670
gaa caa gat tta gaa gca gcg aag aaa gca gtg aat gcc ttg ttt acg			2064
Glu Gln Asp Leu Glu Ala Ala Lys Lys Ala Val Asn Ala Leu Phe Thr			
	675	680	685
aat aca aaa gat ggc tta cga cca ggc gta acg gat tat gaa gtg aat			2112
Asn Thr Lys Asp Gly Leu Arg Pro Gly Val Thr Asp Tyr Glu Val Asn			
	690	695	700
caa gcg gca aac tta gtg gaa tgc cta tcg gat gat ttg tat cca aat			2160

Gln Ala Ala Asn Leu Val Glu Cys Leu Ser Asp Asp Leu Tyr Pro Asn	
705 710 715 720	
gaa aaa cga ttg tta ttt gat gca gtg aga gag gca aaa cgc ctc agt	2208
Glu Lys Arg Leu Leu Phe Asp Ala Val Arg Glu Ala Lys Arg Leu Ser	
725 730 735	
gag gca cgt aat ttg ctt caa gat cca gat ttc caa gag ata aat gga	2256
Glu Ala Arg Asn Leu Leu Gln Asp Pro Asp Phe Gln Glu Ile Asn Gly	
740 745 750	
gaa aat ggc tgg acg gca agt acg gga att gag gtt ata gaa ggg gat	2304
Glu Asn Gly Trp Thr Ala Ser Thr Gly Ile Glu Val Ile Glu Gly Asp	
755 760 765	
gct tta ttc aaa ggg cgt tat cta cgc cta cca ggt gcg aga gaa ata	2352
Ala Leu Phe Lys Gly Arg Tyr Leu Arg Leu Pro Gly Ala Arg Glu Ile	
770 775 780	
gat acg gaa acg tat cca acg tat ctg tat caa aaa gta gag gaa ggt	2400
Asp Thr Glu Thr Tyr Pro Thr Tyr Leu Tyr Gln Lys Val Glu Glu Gly	
785 790 795 800	
gta tta aaa cca tac aca aga tat aga ttg aga ggg ttt gtc gga agc	2448
Val Leu Lys Pro Tyr Thr Arg Tyr Arg Leu Arg Gly Phe Val Gly Ser	
805 810 815	
agt caa gga ttg gaa att ttc aca att cgt cat caa acg aac cga att	2496
Ser Gln Gly Leu Glu Ile Phe Thr Ile Arg His Gln Thr Asn Arg Ile	
820 825 830	
gta aaa aat gta ccg gat gat ttg ctg cca gat gta tct cct gtt aac	2544
Val Lys Asn Val Pro Asp Asp Leu Leu Pro Asp Val Ser Pro Val Asn	
835 840 845	
tcg gat ggt agt atc aat cga tgc agc gaa caa aag tat gtg aat agc	2592
Ser Asp Gly Ser Ile Asn Arg Cys Ser Glu Gln Lys Tyr Val Asn Ser	
850 855 860	
cgt tta gaa gta gaa aac cgt tct ggt gaa gcg cat gag ttc tct att	2640
Arg Leu Glu Val Glu Asn Arg Ser Gly Glu Ala His Glu Phe Ser Ile	
865 870 875 880	
cct att gat aca ggt gaa atc gat tac aat gaa aat gca gga ata tgg	2688
Pro Ile Asp Thr Gly Glu Ile Asp Tyr Asn Glu Asn Ala Gly Ile Trp	
885 890 895	
gtt gga ttt aag att acg gac cca gag gga tat gca aca ctc gga aac	2736
Val Gly Phe Lys Ile Thr Asp Pro Glu Gly Tyr Ala Thr Leu Gly Asn	
900 905 910	
cta gaa ttg gtc gaa gag gga cct tta tca gga gac gca tta gaa cgc	2784
Leu Glu Leu Val Glu Glu Gly Pro Leu Ser Gly Asp Ala Leu Glu Arg	
915 920 925	
ttg caa aga gaa gaa caa cag tgg aag att caa atg aca aga aga cgt	2832
Leu Gln Arg Glu Glu Gln Gln Trp Lys Ile Gln Met Thr Arg Arg Arg	
930 935 940	
gaa gaa aca gat aga agg tat atg gca tcg aaa caa gcg gta gat cgt	2880
Glu Glu Thr Asp Arg Arg Tyr Met Ala Ser Lys Gln Ala Val Asp Arg	
945 950 955 960	



tta tat gcc gat tat cag gat cag caa ctg aat cct gat gta gag att	2928
Leu Tyr Ala Asp Tyr Gln Asp Gln Gln Leu Asn Pro Asp Val Glu Ile	
965 970 975	
aca gat ctt act gcg gcc caa gat ctg ata cag tcc att cct tac gta	2976
Thr Asp Leu Thr Ala Ala Gln Asp Leu Ile Gln Ser Ile Pro Tyr Val	
980 985 990	
tat aac gaa atg ttc cca gaa ata cca ggg atg aac tat acg aag ttt	3024
Tyr Asn Glu Met Phe Pro Gln Ile Pro Gly Met Asn Tyr Thr Lys Phe	
995 1000 1005	
aca gaa tta aca gat cga ctc caa caa gcg tgg agt ttg tat gat cag	3072
Thr Glu Leu Thr Asp Arg Leu Gln Gln Ala Trp Ser Leu Tyr Asp Gln	
1010 1015 1020	
cga aat gcc ata cca aat ggt gat ttt cga aat ggg tta agt aat tgg	3120
Arg Asn Ala Ile Pro Asn Gly Asp Phe Arg Asn Gly Leu Ser Asn Trp	
1025 1030 1035 1040	
aat gca acg cct ggc gta gaa gta caa caa atc aat cat aca tct gtc	3168
Asn Ala Thr Pro Gly Val Glu Val Gln Gln Ile Asn His Thr Ser Val	
1045 1050 1055	
ctt gtg att cca aac tgg gat gag caa gtt tcg caa cag ttt aca gtt	3216
Leu Val Ile Pro Asn Trp Asp Glu Gln Val Ser Gln Gln Phe Thr Val	
1060 1065 1070	
caa ccg aat caa aga tat gtg tta cga gtt act gcg aga aaa gaa ggg	3264
Gln Pro Asn Gln Arg Tyr Val Leu Arg Val Thr Ala Arg Lys Glu Gly	
1075 1080 1085	
gta gga aat gga tat gta agt atc cgt gat ggt gga aat caa aca gaa	3312
Val Gly Asn Gly Tyr Val Ser Ile Arg Asp Gly Gly Asn Gln Thr Glu	
1090 1095 1100	
acg ctt act ttt agt gca agc gat tat gat aca aat gga atg tat aat	3360
Thr Leu Thr Phe Ser Ala Ser Asp Tyr Asp Thr Asn Gly Met Tyr Asn	
1105 1110 1115 1120	
acg caa gtg tcc aat aca aat gga tat aac aca aat aat gcg tat aat	3408
Thr Gln Val Ser Asn Thr Asn Gly Tyr Asn Thr Asn Asn Ala Tyr Asn	
1125 1130 1135	
aca caa gca tcg agt aca aac gga tat aac gca aat aat atg tat aat	3456
Thr Gln Ala Ser Ser Thr Asn Gly Tyr Asn Ala Asn Asn Met Tyr Asn	
1140 1145 1150	
acg caa gca tcg aat aca aac gga tat aac aca aat agt gtg tac aat	3504
Thr Gln Ala Ser Asn Thr Asn Gly Tyr Asn Thr Asn Ser Val Tyr Asn	
1155 1160 1165	
gat caa acc ggc tat atc aca aaa aca gtg aca ttc atc ccg tat aca	3552
Asp Gln Thr Gly Tyr Ile Thr Lys Thr Val Thr Phe Ile Pro Tyr Thr	
1170 1175 1180	
gat caa atg tgg att gag atg agt gag aca gaa ggt aca ttc tat ata	3600
Asp Gln Met Trp Ile Glu Met Ser Glu Thr Glu Gly Thr Phe Tyr Ile	
1185 1190 1195 1200	
gaa agt gta gaa ttg att gta gac gta gag taa	3633
Glu Ser Val Glu Leu Ile Val Asp Val Glu *	
1205 1210	

<210> 4  
 <211> 1210  
 <212> PRT  
 <213> Bacillus thuringiensis

<400> 4  
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
 1 5 10 15  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 20 25 30  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 35 40 45  
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
 50 55 60  
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
 65 70 75 80  
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
 85 90 95  
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp  
 100 105 110  
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
 115 120 125  
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn  
 130 135 140  
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro  
 145 150 155 160  
 Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu  
 165 170 175  
 Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe  
 180 185 190  
 Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu  
 195 200 205  
 Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser  
 210 215 220  
 Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala  
 225 230 235 240  
 Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys  
 245 250 255  
 Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg  
 260 265 270  
 Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn  
 275 280 285  
 Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg  
 290 295 300  
 Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly  
 305 310 315 320  
 Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val  
 325 330 335  
 Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr  
 340 345 350  
 Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala  
 355 360 365  
 Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys  
 370 375 380  
 Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp  
 385 390 395 400  
 Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu  
 405 410 415  
 Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro  
 420 425 430  
 Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr



Glu Glu Thr Asp Arg Arg Tyr Met Ala Ser Lys Gln Ala Val Asp Arg  
 945 950 955 960  
 Leu Tyr Ala Asp Tyr Gln Asp Gln Gln Leu Asn Pro Asp Val Glu Ile  
 965 970 975  
 Thr Asp Leu Thr Ala Ala Gln Asp Leu Ile Gln Ser Ile Pro Tyr Val  
 980 985 990  
 Tyr Asn Glu Met Phe Pro Glu Ile Pro Gly Met Asn Tyr Thr Lys Phe  
 995 1000 1005  
 Thr Glu Leu Thr Asp Arg Leu Gln Gln Ala Trp Ser Leu Tyr Asp Gln  
 1010 1015 1020  
 Arg Asn Ala Ile Pro Asn Gly Asp Phe Arg Asn Gly Leu Ser Asn Trp  
 1025 1030 1035 1040  
 Asn Ala Thr Pro Gly Val Glu Val Gln Gln Ile Asn His Thr Ser Val  
 1045 1050 1055  
 Leu Val Ile Pro Asn Trp Asp Glu Gln Val Ser Gln Gln Phe Thr Val  
 1060 1065 1070  
 Gln Pro Asn Gln Arg Tyr Val Leu Arg Val Thr Ala Arg Lys Glu Gly  
 1075 1080 1085  
 Val Gly Asn Gly Tyr Val Ser Ile Arg Asp Gly Gly Asn Gln Thr Glu  
 1090 1095 1100  
 Thr Leu Thr Phe Ser Ala Ser Asp Tyr Asp Thr Asn Gly Met Tyr Asn  
 1105 1110 1115 1120  
 Thr Gln Val Ser Asn Thr Asn Gly Tyr Asn Thr Asn Asn Ala Tyr Asn  
 1125 1130 1135  
 Thr Gln Ala Ser Ser Thr Asn Gly Tyr Asn Ala Asn Asn Met Tyr Asn  
 1140 1145 1150  
 Thr Gln Ala Ser Asn Thr Asn Gly Tyr Asn Thr Asn Ser Val Tyr Asn  
 1155 1160 1165  
 Asp Gln Thr Gly Tyr Ile Thr Lys Thr Val Thr Phe Ile Pro Tyr Thr  
 1170 1175 1180  
 Asp Gln Met Trp Ile Glu Met Ser Glu Thr Glu Gly Thr Phe Tyr Ile  
 1185 1190 1195 1200  
 Glu Ser Val Glu Leu Ile Val Asp Val Glu  
 1205 1210

<210> 5  
 <211> 2003  
 <212> DNA  
 <213> *Bacillus thuringiensis* (truncated)

<220>  
 <221> CDS  
 <222> (1)...(2001)  
 <221> misc\_feature  
 <222> (0)...(0)  
 <223> 1218-1

<400> 5  
 atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48  
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
 1 5 10 15  
 tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 20 25 30  
 cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 35 40 45  
 tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192

Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val		
50						55					60						
agc	gga	caa	gat	gca	gct	aag	gcc	gca	att	gat	ata	gta	ggg	aaa	tta	240	
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu	80	
65					70				75								
cta	tca	ggg	tta	ggg	gtc	cca	ttt	gtt	ggg	ccg	ata	gtg	agt	ctt	tat	288	
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr	95	
				85					90								
act	caa	ctt	att	gat	att	ctg	tgg	cct	tca	ggg	gaa	aag	agt	caa	tgg	336	
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp	110	
			100					105									
gaa	att	ttt	atg	gaa	caa	gta	gaa	gaa	ctc	att	aat	caa	aaa	ata	gca	384	
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala	125	
		115						120									
gaa	tat	gca	agg	aat	aaa	gcg	ctt	tgc	gaa	tta	gaa	gga	tta	ggg	aat	432	
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn	140	
		130				135											
aat	tac	caa	tta	tat	cta	act	gcg	ctt	gaa	gaa	tgg	gaa	gaa	aat	cca	480	
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro	160	
					150						155						
aat	ggg	tca	aga	gcc	tta	cga	gat	gtg	cga	aat	cga	ttt	gaa	atc	ctg	528	
Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg	Phe	Glu	Ile	Leu	175	
				165					170								
gat	agt	tta	ttt	acg	caa	tat	atg	cca	tct	ttt	aga	gtg	aca	aat	ttt	576	
Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg	Val	Thr	Asn	Phe	190	
			180						185								
gaa	gta	cca	ttc	ctt	act	gta	tat	gca	atg	gca	gcc	aac	ctt	cat	tta	624	
Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	Asn	Leu	His	Leu	205	
		195						200									
ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	gaa	gaa	tgg	gga	tgg	tca	672	
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	Trp	Ser	220	
		210					215										
aca	act	act	att	aat	aac	tat	tat	gat	cgt	caa	atg	aaa	ctt	act	gca	720	
Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	Ala	240	
					230						235						
gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	gaa	act	ggg	tta	gca	aaa	768	
Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	Ala	Lys	255	
				245					250								
tta	aaa	ggc	acg	agc	gct	aaa	caa	tgg	gtt	gac	tat	aac	caa	ttc	cgt	816	
Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	Arg	270	
			260						265								
aga	gaa	atg	aca	ctg	gcg	gtt	tta	gat	gtt	gtt	gca	tta	ttc	cca	aat	864	
Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Asn	285	
		275						280									
tat	gac	aca	cgc	acg	tac	cca	atg	gaa	acg	aaa	gca	caa	cta	aca	agg	912	
Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg	300	
		290					295										

gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca att ggt	960
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly	
305 310 315 320	
tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca tcc gtt	1008
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val	
325 330 335	
att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg tat	1056
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr	
340 345 350	
aca caa tca aga agc att tct tcc gct cgc tat ata aga cat tgg gct	1104
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala	
355 360 365	
ggg cat caa ata agc tac cat cgt gtc agt agg ggt agt aat ctt caa	1152
Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln	
370 375 380	
caa atg tat gga act aat caa aat cta cac agc act agt acc ttt gat	1200
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp	
385 390 395 400	
ttt acg aat tat gat att tac aag act cta tca aag gat gca gta ctc	1248
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu	
405 410 415	
ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga atg cca	1296
Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro	
420 425 430	
gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga aag acg	1344
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr	
435 440 445	
tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca aga gat	1392
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp	
450 455 460	
tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat tat gag	1440
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu	
465 470 475 480	
tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg ggt	1488
Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly	
485 490 495	
aac act acc gga tta gta cct gta ttt tct tgg aca cat cga agt gca	1536
Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala	
500 505 510	
gat tta aac aat aca ata tat tca gat aaa atc act caa att ccg gcc	1584
Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala	
515 520 525	
gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa gga cca	1632
Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro	
530 535 540	
gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt tct	1680
Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser	
545 550 555 560	

gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa aaa gca	1728
Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala	
565 570 575	
ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat att gta	1776
Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val	
580 585 590	
ttg cat gta aac gat gct cag att cag atg cca aaa aca atg aac cca	1824
Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro	
595 600 605	
ggg gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc aca	1872
Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr	
610 615 620	
aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat tta	1920
Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu	
625 630 635 640	
ggg gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac cga	1968
Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg	
645 650 655	
atc gaa ttc atc cca gta gat gag aca tat gaa gc	2003
Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu	
660 665	

<210> 6  
 <211> 667  
 <212> PRT  
 <213> Bacillus thuringiensis (truncated)

<400> 6

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu	
165 170 175	
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe	
180 185 190	
Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu	
195 200 205	
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser	

210	215	220
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala		
225	230	235
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys		
	245	250
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg		
	260	265
Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn		
	275	280
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg		
	290	295
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly		
305	310	315
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val		
	325	330
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr		
	340	345
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala		
	355	360
Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln		
	370	375
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp		
385	390	395
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu		
	405	410
Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro		
	420	425
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr		
	435	440
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp		
	450	455
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu		
465	470	475
Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly		
	485	490
Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala		
	500	505
Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala		
	515	520
Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro		
	530	535
Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser		
545	550	555
Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala		
	565	570
Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val		
	580	585
Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro		
	595	600
Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr		
	610	615
Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu		
625	630	635
Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg		
	645	650
Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu		
	660	665

<210> 7  
 <211> 2003  
 <212> DNA  
 <213> Bacillus thuringiensis (truncated)



<220>  
 <221> CDS  
 <222> (1)...(2001)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> 1218-2

```

<400> 7
atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50 55 60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85 90 95

act caa ctt att gat att ctg tgg cct tca ggg caa aag agt caa tgg 336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp
100 105 110

gag att ttt atg gaa caa gta gaa gaa ctc ata aat caa aaa ata gca 384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115 120 125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg aaa gaa aat cca 480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro
145 150 155 160

aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt gaa atc ctg 528
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
165 170 175

gat agt tta ttt acg caa tac atg cca tct ttt cga gtg aca aat ttt 576
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
180 185 190

gaa gta cca ttc ctt aca gta tat aca cag gca gcc aac ctt cat tta 624
Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu
195 200 205

ctg tta tta aag gac gct tca att ttt gga gaa gaa tgg gga tgg tct 672

```

Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	Trp	Ser		
210						215					220						
aca	acc	act	att	aat	aac	tat	tat	gat	cgt	caa	atg	aaa	ctt	act	gca	720	
Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	Ala	240	
225					230					235							
gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	gaa	act	ggt	tta	gca	aaa	768	
Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	Ala	Lys	255	
				245					250								
tta	aaa	ggc	acg	agc	gct	aaa	caa	tgg	gtc	gac	tat	aac	caa	ttc	cgt	816	
Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	Arg	270	
			260					265									
aga	gaa	atg	aca	ctg	acg	gtt	tta	gat	gtt	gtt	gca	tta	ttc	cca	aat	864	
Arg	Glu	Met	Thr	Leu	Thr	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Asn	285	
			275					280									
tat	gac	aca	cgc	acg	tac	cca	atg	gaa	acg	aaa	gca	caa	cta	aca	agg	912	
Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg	300	
			290				295										
gaa	gta	tat	aca	gat	cca	ctg	ggc	gcg	gta	aac	gtg	tct	tca	att	ggt	960	
Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	Ile	Gly	320	
					310					315							
tcc	tgg	tat	gac	aaa	gca	cct	tct	ttc	gga	gtg	ata	gaa	tca	tcc	gtt	1008	
Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	Ser	Val	335	
				325					330								
att	cga	cca	ccc	cat	gta	ttt	gat	tat	ata	acg	gga	ctc	aca	gtg	tat	1056	
Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	Val	Tyr	350	
			340					345									
aca	caa	tca	aga	agc	att	tct	tcc	gct	cgc	tat	ata	aga	cat	tgg	gct	1104	
Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	Ala	365	
			355				360										
ggt	cat	caa	ata	agc	tat	cat	cgg	att	ttt	agt	gat	aat	att	ata	aaa	1152	
Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Ile	Phe	Ser	Asp	Asn	Ile	Ile	Lys	380	
			370				375										
cag	atg	tat	gga	act	aat	caa	aat	cta	cac	agc	act	agt	acc	ttt	gat	1200	
Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	Phe	Asp	400	
					390					395							
ttt	acg	aat	tat	gat	att	tac	aag	acg	tta	tca	aaa	gat	gcg	gtg	ctc	1248	
Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu	415	
				405					410								
ctt	gat	att	gtt	ttt	cct	ggt	tat	acg	tat	ata	ttt	ttt	gga	atg	cca	1296	
Leu	Asp	Ile	Val	Phe	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	Pro	430	
				420				425									
gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	aat	aat	acc	aga	aag	acg	1344	
Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	Thr	445	
			435				440										
tta	aag	tat	aat	ccg	gtt	tcc	aaa	gat	att	ata	gcg	ggg	aca	aga	gat	1392	
Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	Gly	Thr	Arg	Asp	460	
			450				455										

tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat tat gag	1440
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu	
465 470 475 480	
tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg ggt	1488
Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly	
485 490 495	
tca act acc gga tta gta cct gta ttt tct tgg aca cat cgg agt gcc	1536
Ser Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala	
500 505 510	
gat ctt ata aat gca gtt cat tca gat aaa att act cag att ccg gtc	1584
Asp Leu Ile Asn Ala Val His Ser Asp Lys Ile Thr Gln Ile Pro Val	
515 520 525	
gta aag gtt tct gat ttg gct ccc tct ata aca gga ggg cca aat aat	1632
Val Lys Val Ser Asp Leu Ala Pro Ser Ile Thr Gly Gly Pro Asn Asn	
530 535 540	
acc gtt gta tcg ggt cct gga ttt aca ggg ggg ggg ata ata aaa gta	1680
Thr Val Val Ser Gly Pro Gly Phe Thr Gly Gly Gly Ile Ile Lys Val	
545 550 555 560	
ata aga aat gga gta att ata tca cat atg cgt gtt aaa att tca gac	1728
Ile Arg Asn Gly Val Ile Ile Ser His Met Arg Val Lys Ile Ser Asp	
565 570 575	
att aac aaa gaa tat agt atg agg att cgg tat gct tcc gct aat aat	1776
Ile Asn Lys Glu Tyr Ser Met Arg Ile Arg Tyr Ala Ser Ala Asn Asn	
580 585 590	
act gaa ttt tat ata aat cct tct gaa gaa aac gtt aaa tct cac gct	1824
Thr Glu Phe Tyr Ile Asn Pro Ser Glu Glu Asn Val Lys Ser His Ala	
595 600 605	
caa aaa act atg aat aga ggt gaa gct tta aca tat aat aaa ttt aat	1872
Gln Lys Thr Met Asn Arg Gly Glu Ala Leu Thr Tyr Asn Lys Phe Asn	
610 615 620	
tat gcg act ttg ccc cct att aaa ttt acg aca acc gaa cct ttc att	1920
Tyr Ala Thr Leu Pro Pro Ile Lys Phe Thr Thr Thr Glu Pro Phe Ile	
625 630 635 640	
act cta ggg gct ata ttt gaa gcg gaa gac ttt ctt gga att gaa gct	1968
Thr Leu Gly Ala Ile Phe Glu Ala Glu Asp Phe Leu Gly Ile Glu Ala	
645 650 655	
tat ata gac cga atc gaa ttt atc cca gta gat ga	2003
Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Asp	
660 665	

<210> 8

<211> 667

<212> PRT

<213> Bacillus thuringiensis (truncated)

<400> 8

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	

Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met
		35					40					45			
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val
		50				55					60				
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu
		65				70				75				80	
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr
			85						90					95	
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Gln	Lys	Ser	Gln	Trp
			100					105					110		
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala
		115					120					125			
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn
		130				135					140				
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Lys	Glu	Asn	Pro
		145			150						155			160	
Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg	Phe	Glu	Ile	Leu
			165					170						175	
Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg	Val	Thr	Asn	Phe
			180					185					190		
Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Thr	Gln	Ala	Ala	Asn	Leu	His	Leu
		195					200					205			
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	Trp	Ser
		210				215					220				
Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	Ala
		225			230					235				240	
Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	Ala	Lys
			245					250						255	
Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	Arg
		260						265					270		
Arg	Glu	Met	Thr	Leu	Thr	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Asn
		275					280					285			
Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg
		290				295					300				
Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	Ile	Gly
		305			310					315				320	
Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	Ser	Val
			325					330						335	
Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	Val	Tyr
			340					345						350	
Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	Ala
		355				360						365			
Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Ile	Phe	Ser	Asp	Asn	Ile	Ile	Lys
		370				375					380				
Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	Phe	Asp
		385			390					395				400	
Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu
			405					410						415	
Leu	Asp	Ile	Val	Phe	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	Pro
			420					425					430		
Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	Thr
		435					440					445			
Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	Gly	Thr	Arg	Asp
		450				455					460				
Ser	Glu	Leu	Glu	Leu	Pro	Glu	Thr	Ser	Asp	Gln	Pro	Asn	Tyr	Glu	
		465			470				475					480	
Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	Pro	Ala	Thr	Gly
			485					490						495	
Ser	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala
			500					505					510		
Asp	Leu	Ile	Asn	Ala	Val	His	Ser	Asp	Lys	Ile	Thr	Gln	Ile	Pro	Val
		515					520					525			
Val	Lys	Val	Ser	Asp	Leu	Ala	Pro	Ser	Ile	Thr	Gly	Gly	Pro	Asn	Asn

530 535 540  
 Thr Val Val Ser Gly Pro Gly Phe Thr Gly Gly Gly Ile Ile Lys Val  
 545 550 555 560  
 Ile Arg Asn Gly Val Ile Ile Ser His Met Arg Val Lys Ile Ser Asp  
 565 570 575  
 Ile Asn Lys Glu Tyr Ser Met Arg Ile Arg Tyr Ala Ser Ala Asn Asn  
 580 585 590  
 Thr Glu Phe Tyr Ile Asn Pro Ser Glu Glu Asn Val Lys Ser His Ala  
 595 600 605  
 Gln Lys Thr Met Asn Arg Gly Glu Ala Leu Thr Tyr Asn Lys Phe Asn  
 610 615 620  
 Tyr Ala Thr Leu Pro Pro Ile Lys Phe Thr Thr Thr Glu Pro Phe Ile  
 625 630 635 640  
 Thr Leu Gly Ala Ile Phe Glu Ala Glu Asp Phe Leu Gly Ile Glu Ala  
 645 650 655  
 Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Asp  
 660 665

<210> 9  
 <211> 2010  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)...(2010)  
 <223> Maize optimized Cry1218-1

<221> misc\_feature  
 <222> (0)...(0)  
 <223> mol1218-1

<400> 9  
 atg tcc ccc aac aac cag aac gag tac gag atc atc gac gcc acc ccc 48  
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
 1 5 10 15  
 tcc acc tcc gtg tcc aac gac tcc aac cgc tac ccc ttc gcc aac gag 96  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 20 25 30  
 ccc acc aac gcc ctc cag aac atg gac tac aag gac tac ctc aag atg 144  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 35 40 45  
 tcc gcc ggc aac gcc tcc gag tac ccc ggc tcc ccc gag gtg ctc gtg 192  
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
 50 55 60  
 tcc ggc cag gac gcc gcc aag gcc gcc atc gac atc gtg ggc aag ctc 240  
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
 65 70 75 80  
 ctc tcc ggc ctc ggc gtg ccc ttc gtg ggc ccc atc gtg tcc ctc tac 288  
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
 85 90 95  
 acc cag ctc atc gac atc ctc tgg ccc tcc ggc gag aag tcc cag tgg 336  
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp  
 100 105 110

gaa atc ttc atg gag cag gtg gag gag ctc atc aac cag aag atc gcc	384
Glu Ile Phe Met Glu Gln Val Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gag tac gcc cgc aac aag gcc ctc tcc gag ctg gag ggc ctc ggc aac	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aac tac cag ctc tac ctc acc gcc ctg gag gag tgg gag gag aac ccc	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
aac ggc tcc cgc gcc ctc cgc gac gtg cgc aac cgc ttc gag atc ctc	528
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu	
165 170 175	
gac tcc ctc ttc acc cag tac atg ccc tcc ttc cgc gtg acc aac ttc	576
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe	
180 185 190	
gag gtg ccc ttc ctc acc gtg tac gcc atg gcc gcc aac ctc cac ctc	624
Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu	
195 200 205	
ctc ctc ctc aag gac gcc tcc atc ttc ggc gag gag tgg ggc tgg tcc	672
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser	
210 215 220	
acc acc acc atc aac aac tac tac gac cgc cag atg aag ctc acc gcc	720
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala	
225 230 235 240	
gag tac tcc gac cac tgc gtg aag tgg tat gag acc ggc ctc gcc aag	768
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys	
245 250 255	
ctc aag ggc acc tcc gcc aag cag tgg gtg gac tac aac cag ttc cgc	816
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg	
260 265 270	
cgc gag atg acc ctc gcc gtg ctc gac gtg gtg gcc ctc ttc ccc aac	864
Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn	
275 280 285	
tac gac acc cgc acc tac ccc atg gag acc aag gcc cag ctc acc cgc	912
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg	
290 295 300	
gag gtg tac acc gac ccg ctc ggc gcc gtg aac gtg tcc tcc atc gcc	960
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly	
305 310 315 320	
tct tgg tac gac aag gcc cca agc ttc ggc gtg atc gag tcc tcc gtg	1008
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val	
325 330 335	
atc cgc ccg ccg cac gtg ttc gac tac atc acc ggc ctc acc gtg tac	1056
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr	
340 345 350	
acc cag tcc cgc tcc atc tcc tcc gcc cgc tac atc cgc cac tgg gcc	1104
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala	
355 360 365	

ggc cac cag atc tcc tac cac cgc gtg tcc cgc ggc tcc aac ctc cag	1152
Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln	
370 375 380	
cag atg tac ggc acc aac cag aac ctc cac tcc acc tcc acc ttc gac	1200
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp	
385 390 395 400	
ttc acc aac tac gac atc tac aag acc ctc tcc aag gac gcc gtg ctc	1248
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu	
405 410 415	
ctc gac atc gtg tac ccc ggc tac acc tac atc ttc ttc ggc atg ccg	1296
Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro	
420 425 430	
gag gtg gag ttc ttc atg gtg aac cag ctc aac aac acc cgc aag acc	1344
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr	
435 440 445	
ctc aaa tac aac ccc gtg tcc aag gac atc atc gcc tcc acc cgc gac	1392
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp	
450 455 460	
tcc gag ctc gag ctc ccc ccc gag acc tcc gac cag ccc aac tac gag	1440
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu	
465 470 475 480	
tcc tac tcc cac cgc ctc tgc cac atc acc tcc atc ccc gcc acc ggc	1488
Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly	
485 490 495	
aac acc acc ggc ctc gtg ccg gtg ttc tcc tgg acc cac cgc tct gca	1536
Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala	
500 505 510	
gac ctc aac aac acc atc tac tcc gac aag atc acc cag atc ccc gcc	1584
Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala	
515 520 525	
gtg aag tgc tgg gac aac ctc ccc ttc gtg ccc gtg gtg aag ggc ccc	1632
Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro	
530 535 540	
ggc cac acc ggc ggc gac ctc ctc cag tac aac cgc tcc acc ggc tcc	1680
Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser	
545 550 555 560	
gtg ggc acc ctc ttc ctc gcc cgc tac ggc ctc gcc ctg gag aag gcc	1728
Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala	
565 570 575	
ggc aag tac cgc gtg cgc ctc cgc tac gcc act gac gcc gac atc gtg	1776
Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val	
580 585 590	
ctc cac gtg aac gac gcc cag atc cag atg ccc aag acc atg aac ccc	1824
Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro	
595 600 605	
ggc gag gac ctc acc tcc aag acc ttc aag gtg gcc gac gcc atc acc	1872
Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr	

610	615	620	
acc ctc aac ctc gcc acc gac tcc tcc ctc gcc ctc aag cac aac ctc			1920
Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu			
625	630	635	640
ggc gag gac ccc aac tcc acc ctc tcc ggc atc gtg tac gtg gac cgc			1968
Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg			
	645	650	655
atc gag ttc atc ccc gtg gac gag acc tac gag gcc gag tga			2010
Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu *			
	660	665	

<210> 10  
 <211> 669  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Maize optimized Cry1218-1

<400> 10  
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
 1 5 10 15  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 20 25 30  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 35 40 45  
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
 50 55 60  
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
 65 70 75 80  
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
 85 90 95  
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp  
 100 105 110  
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
 115 120 125  
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn  
 130 135 140  
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro  
 145 150 155 160  
 Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu  
 165 170 175  
 Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe  
 180 185 190  
 Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu  
 195 200 205  
 Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser  
 210 215 220  
 Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala  
 225 230 235 240  
 Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys  
 245 250 255  
 Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg  
 260 265 270  
 Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn  
 275 280 285  
 Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg  
 290 295 300



Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly  
 305 310 315 320  
 Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val  
 325 330 335  
 Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr  
 340 345 350  
 Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala  
 355 360 365  
 Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu Gln  
 370 375 380  
 Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp  
 385 390 395 400  
 Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu  
 405 410 415  
 Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro  
 420 425 430  
 Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr  
 435 440 445  
 Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg Asp  
 450 455 460  
 Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu  
 465 470 475 480  
 Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly  
 485 490 495  
 Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala  
 500 505 510  
 Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro Ala  
 515 520 525  
 Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly Pro  
 530 535 540  
 Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser  
 545 550 555 560  
 Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala  
 565 570 575  
 Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val  
 580 585 590  
 Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro  
 595 600 605  
 Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr  
 610 615 620  
 Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu  
 625 630 635 640  
 Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg  
 645 650 655  
 Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu  
 660 665

<210> 11  
 <211> 2022  
 <212> DNA  
 <213> Bacillus thuringiensis (mutated)

<220>  
 <221> CDS  
 <222> (1)...(2022)  
 <221> misc\_feature  
 <222> (0)...(0)  
 <223> NGS.R.N1218-1

<400> 11  
 atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48

Met	Ser	Pro	Asn	Asn	Gln	Asn	Glu	Tyr	Glu	Ile	Ile	Asp	Ala	Thr	Pro		
1				5					10					15			
tct	act	tct	gta	tcc	aat	gat	tct	aac	aga	tac	cct	ttt	gcg	aat	gag	96	
Ser	Thr	Ser	Val	Ser	Asn	Asp	Ser	Asn	Arg	Tyr	Pro	Phe	Ala	Asn	Glu		
			20					25					30				
cca	aca	aat	gcg	cta	caa	aat	atg	gat	tat	aaa	gat	tat	tta	aaa	atg	144	
Pro	Thr	Asn	Ala	Leu	Gln	Asn	Met	Asp	Tyr	Lys	Asp	Tyr	Leu	Lys	Met		
		35					40					45					
tct	gcg	gga	aat	gct	agt	gaa	tac	cct	ggg	tca	cct	gaa	gta	ctt	gtt	192	
Ser	Ala	Gly	Asn	Ala	Ser	Glu	Tyr	Pro	Gly	Ser	Pro	Glu	Val	Leu	Val		
	50					55					60						
agc	gga	caa	gat	gca	gct	aag	gcc	gca	att	gat	ata	gta	ggg	aaa	tta	240	
Ser	Gly	Gln	Asp	Ala	Ala	Lys	Ala	Ala	Ile	Asp	Ile	Val	Gly	Lys	Leu		
	65					70				75					80		
cta	tca	ggg	tta	ggg	gtc	cca	ttt	gtt	ggg	ccg	ata	gtg	agt	ctt	tat	288	
Leu	Ser	Gly	Leu	Gly	Val	Pro	Phe	Val	Gly	Pro	Ile	Val	Ser	Leu	Tyr		
				85					90					95			
act	caa	ctt	att	gat	att	ctg	tgg	cct	tca	ggg	gaa	aag	agt	caa	tgg	336	
Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	Trp		
			100					105					110				
gaa	att	ttt	atg	gaa	caa	gta	gaa	gaa	ctc	att	aat	caa	aaa	ata	gca	384	
Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	Ala		
		115					120					125					
gaa	tat	gca	agg	aat	aaa	gcg	ctt	tcg	gaa	tta	gaa	gga	tta	ggg	aat	432	
Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	Asn		
		130				135						140					
aat	tac	caa	tta	tat	cta	act	gcg	ctt	gaa	gaa	tgg	gaa	gaa	aat	cca	480	
Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	Pro		
					150						155				160		
aat	ggg	tca	aga	aat	ggg	tcc	cgg	gcc	tta	cga	gat	gtg	cga	aat	cga	528	
Asn	Gly	Ser	Arg	Asn	Gly	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg		
				165				170						175			
ttt	gaa	atc	ctg	gat	agt	tta	ttt	acg	caa	tat	atg	cca	tct	ttt	aga	576	
Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg		
			180					185					190				
gtg	aca	aat	ttt	gaa	gta	cca	ttc	ctt	act	gta	tat	gca	atg	gca	gcc	624	
Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala		
		195					200					205					
aac	ctt	cat	tta	ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	gaa	gaa	672	
Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu		
		210					215				220						
tgg	gga	tgg	tca	aca	act	act	att	aat	aac	tat	tat	gat	cgt	caa	atg	720	
Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met		
		225				230				235					240		
aaa	ctt	act	gca	gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	gaa	act	768	
Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr		
				245				250						255			

ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	

cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca	1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg	1920
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu	
625 630 635 640	
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg	2016
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gaa taa	2022
Glu *	

<210> 12  
 <211> 673  
 <212> PRT  
 <213> *Bacillus thuringiensis* (mutated)

<400> 12  
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
 1 5 10 15  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 20 25 30  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 35 40 45  
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
 50 55 60  
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
 65 70 75 80  
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr



Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys  
595 600 605  
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala  
610 615 620  
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu  
625 630 635 640  
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val  
645 650 655  
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala  
660 665 670  
Glu

<210> 13  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>

<223> NGSr Insert

<400> 13  
aatggttccc gg

12

<210> 14  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> NGSr Insert

<400> 14  
Asn Gly Ser Arg  
1

<210> 15  
<211> 2010  
<212> DNA  
<213> Bacillus thuringiensis (truncated)

<220>  
<221> CDS  
<222> (1)...(2010)

<221> misc\_feature  
<222> (0)...(0)  
<223> 1218-1A

<400> 15  
atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48  
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96  
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144  
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met

35	40	45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt			192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val			
50	55	60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta			240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu			
65	70	75	80
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat			288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr			
	85	90	95
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg			336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp			
	100	105	110
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca			384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala			
	115	120	125
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat			432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn			
	130	135	140
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca			480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro			
	145	150	155
aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt gaa atc ctg			528
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu			
	165	170	175
gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca aat ttt			576
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe			
	180	185	190
gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt cat tta			624
Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His Leu			
	195	200	205
ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga tgg tca			672
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser			
	210	215	220
aca act act att aat aac tat tat gat cgt caa atg aaa ctt act gca			720
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala			
	225	230	235
gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca aaa			768
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys			
	245	250	255
tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa ttc cgt			816
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg			
	260	265	270
aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc cca aat			864
Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro Asn			
	275	280	285
tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca agg			912

Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg		
290						295					300						
gaa	gta	tat	aca	gat	cca	ctg	ggc	gcg	gta	aac	gtg	tct	tca	att	ggg	960	
Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	Ile	Gly		
305					310					315					320		
tcc	tgg	tat	gac	aaa	gca	cct	tct	ttc	gga	gtg	ata	gaa	tca	tcc	gtt	1008	
Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	Ser	Val		
				325					330					335			
att	cga	cca	ccc	cat	gta	ttt	gat	tat	ata	acg	gga	ctc	aca	gtg	tat	1056	
Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	Val	Tyr		
				340				345						350			
aca	caa	tca	aga	agc	att	tct	tcc	gct	cgc	tat	ata	aga	cat	tgg	gct	1104	
Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	Ala		
				355				360						365			
ggg	cat	caa	ata	agc	tac	cat	cgt	gtc	agt	agg	ggg	agt	aat	ctt	caa	1152	
Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	Ser	Asn	Leu	Gln		
				370				375						380			
caa	atg	tat	gga	act	aat	caa	aat	cta	cac	agc	act	agt	acc	ttt	gat	1200	
Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	Phe	Asp		
					390					395					400		
ttt	acg	aat	tat	gat	att	tac	aag	act	cta	tca	aag	gat	gca	gta	ctc	1248	
Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu		
				405					410						415		
ctt	gat	att	gtt	tac	cct	ggg	tat	acg	tat	ata	ttt	ttt	gga	atg	cca	1296	
Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	Pro		
				420				425						430			
gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	aat	aat	acc	aga	aag	acg	1344	
Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	Thr		
			435				440							445			
tta	aag	tat	aat	cca	gtt	tcc	aaa	gat	att	ata	gcg	agt	aca	aga	gat	1392	
Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	Ser	Thr	Arg	Asp		
						455					460						
tcg	gaa	tta	gaa	tta	cct	cca	gaa	act	tca	gat	caa	cca	aat	tat	gag	1440	
Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln	Pro	Asn	Tyr	Glu		
					470					475					480		
tca	tat	agc	cat	aga	tta	tgt	cat	atc	aca	agt	att	ccc	gcg	acg	ggg	1488	
Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	Pro	Ala	Thr	Gly		
				485					490						495		
aac	act	acc	gga	tta	gta	cct	gta	ttt	tct	tgg	aca	cat	cga	agt	gca	1536	
Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala		
				500				505						510			
gat	tta	aac	aat	aca	ata	tat	tca	gat	aaa	atc	act	caa	att	ccg	gcc	1584	
Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	Gln	Ile	Pro	Ala		
				515				520						525			
gtt	aaa	tgt	tgg	gat	aat	tta	ccg	ttt	gtt	cca	gtg	gta	aaa	gga	cca	1632	
Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val	Val	Lys	Gly	Pro		
				530			535							540			



```

gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt tct 1680
Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly Ser
545                    550                    555                    560

gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa aaa gca 1728
Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys Ala
                    565                    570                    575

ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat att gta 1776
Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile Val
                    580                    585                    590

ttg cat gta aac gat gct cag att cag atg cca aaa aca atg aac cca 1824
Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn Pro
                    595                    600                    605

ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc aca 1872
Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile Thr
610                    615                    620

aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat tta 1920
Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn Leu
625                    630                    635                    640

ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac cga 1968
Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp Arg
                    645                    650                    655

atc gaa ttc atc cca gta gat gag aca tat gaa gcg gaa taa 2010
Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu *
                    660                    665

```

```

<210> 16
<211> 669
<212> PRT
<213> Bacillus thuringiensis (truncated)

```

```

<400> 16
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
1          5          10          15
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
20          25          30
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
35          40          45
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
50          55          60
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
65          70          75          80
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
85          90          95
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
100         105         110
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115         120         125
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130         135         140
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
145         150         155         160
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
165         170         175
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe

```

			180						185						190					
Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	Asn	Leu	His	Leu					
		195					200					205								
Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	Trp	Ser					
	210					215					220									
Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	Ala					
225					230					235					240					
Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	Ala	Lys					
				245					250					255						
Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	Arg					
			260					265				270								
Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	Asn					
		275					280					285								
Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	Arg					
	290				295						300									
Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	Ile	Gly					
305				310						315					320					
Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	Ser	Val					
				325					330					335						
Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	Val	Tyr					
			340					345					350							
Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	Ala					
		355					360					365								
Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	Ser	Asn	Leu	Gln					
	370				375						380									
Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	Phe	Asp					
385				390						395					400					
Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	Leu					
			405					410						415						
Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	Pro					
			420					425					430							
Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	Thr					
		435					440					445								
Leu	Lys	Tyr	Asn	Pro	Val	Ser	Lys	Asp	Ile	Ile	Ala	Ser	Thr	Arg	Asp					
	450					455					460									
Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln	Pro	Asn	Tyr	Glu					
465				470						475					480					
Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	Pro	Ala	Thr	Gly					
			485					490						495						
Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala					
			500					505				510								
Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	Gln	Ile	Pro	Ala					
		515					520					525			</					

<210> 17  
 <211> 2022  
 <212> DNA  
 <213> *Bacillus thuringiensis* (truncated)

<220>  
 <221> CDS  
 <222> (1)...(2022)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> 1218-2A

```

<400> 17
atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
  1          5          10          15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
          20          25          30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
          35          40          45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
          50          55          60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
          65          70          75          80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
          85          90          95

act caa ctt att gat att ctg tgg cct tca ggg caa aag agt caa tgg 336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp
          100          105          110

gag att ttt atg gaa caa gta gaa gaa ctc ata aat caa aaa ata gca 384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
          115          120          125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
          130          135          140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg aaa gaa aat cca 480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro
          145          150          155          160

aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt gaa atc ctg 528
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu
          165          170          175

gat agt tta ttt acg caa tac atg cca tct ttt cga gtg aca aat ttt 576
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe
          180          185          190

gaa gta cca ttc ctt aca gta tat aca cag gca gcc aac ctt cat tta 624

```

Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu	
195 200 205	
ctg tta tta aag gac gct tca att ttt gga gaa gaa tgg gga tgg tct	672
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser	
210 215 220	
aca acc act att aat aac tat tat gat cgt caa atg aaa ctt act gca	720
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala	
225 230 235 240	
gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca aaa	768
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys	
245 250 255	
tta aaa ggc acg agc gct aaa caa tgg gtc gac tat aac caa ttc cgt	816
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg	
260 265 270	
aga gaa atg aca ctg acg gtt tta gat gtt gtt gca tta ttc cca aat	864
Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn	
275 280 285	
tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca agg	912
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg	
290 295 300	
gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca att ggt	960
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly	
305 310 315 320	
tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca tcc gtt	1008
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val	
325 330 335	
att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg tat	1056
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr	
340 345 350	
aca caa tca aga agc att tct tcc gct cgc tat ata aga cat tgg gct	1104
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala	
355 360 365	
ggt cat caa ata agc tat cat cgg att ttt agt gat aat att ata aaa	1152
Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys	
370 375 380	
cag atg tat gga act aat caa aat cta cac agc act agt acc ttt gat	1200
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp	
385 390 395 400	
ttt acg aat tat gat att tac aag acg tta tca aaa gat gcg gtg ctc	1248
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu	
405 410 415	
ctt gat att gtt ttt cct ggt tat acg tat ata ttt ttt gga atg cca	1296
Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro	
420 425 430	
gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga aag acg	1344
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr	
435 440 445	

tta aag tat aat ccg gtt tcc aaa gat att ata gcg ggg aca aga gat	1392
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Gly Thr Arg Asp	
450 455 460	
tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat tat gag	1440
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu	
465 470 475 480	
tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg ggt	1488
Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr Gly	
485 490 495	
tca act acc gga tta gta cct gta ttt tct tgg aca cat cgg agt gcc	1536
Ser Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser Ala	
500 505 510	
gat ctt ata aat gca gtt cat tca gat aaa att act cag att ccg gtc	1584
Asp Leu Ile Asn Ala Val His Ser Asp Lys Ile Thr Gln Ile Pro Val	
515 520 525	
gta aag gtt tct gat ttg gct ccc tct ata aca gga ggg cca aat aat	1632
Val Lys Val Ser Asp Leu Ala Pro Ser Ile Thr Gly Gly Pro Asn Asn	
530 535 540	
acc gtt gta tcg ggt cct gga ttt aca ggg ggg ggg ata ata aaa gta	1680
Thr Val Val Ser Gly Pro Gly Phe Thr Gly Gly Gly Ile Ile Lys Val	
545 550 555 560	
ata aga aat gga gta att ata tca cat atg cgt gtt aaa att tca gac	1728
Ile Arg Asn Gly Val Ile Ile Ser His Met Arg Val Lys Ile Ser Asp	
565 570 575	
att aac aaa gaa tat agt atg agg att cgg tat gct tcc gct aat aat	1776
Ile Asn Lys Glu Tyr Ser Met Arg Ile Arg Tyr Ala Ser Ala Asn Asn	
580 585 590	
act gaa ttt tat ata aat cct tct gaa gaa aac gtt aaa tct cac gct	1824
Thr Glu Phe Tyr Ile Asn Pro Ser Glu Glu Asn Val Lys Ser His Ala	
595 600 605	
caa aaa act atg aat aga ggt gaa gct tta aca tat aat aaa ttt aat	1872
Gln Lys Thr Met Asn Arg Gly Glu Ala Leu Thr Tyr Asn Lys Phe Asn	
610 615 620	
tat gcg act ttg ccc cct att aaa ttt acg aca acc gaa cct ttc att	1920
Tyr Ala Thr Leu Pro Pro Ile Lys Phe Thr Thr Thr Glu Pro Phe Ile	
625 630 635 640	
act cta ggg gct ata ttt gaa gcg gaa gac ttt ctt gga att gaa gct	1968
Thr Leu Gly Ala Ile Phe Glu Ala Glu Asp Phe Leu Gly Ile Glu Ala	
645 650 655	
tat ata gac cga atc gaa ttt atc cca gta gat gag aca tat gaa gcg	2016
Tyr Ile Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala	
660 665 670	
gaa taa	2022
Glu *	

<210> 18  
<211> 673

<212> PRT

<213> *Bacillus thuringiensis* (truncated)

<400> 18

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
1 5 10 15  
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
20 25 30  
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
35 40 45  
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
50 55 60  
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
65 70 75 80  
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
85 90 95  
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Gln Lys Ser Gln Trp  
100 105 110  
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
115 120 125  
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn  
130 135 140  
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Lys Glu Asn Pro  
145 150 155 160  
Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile Leu  
165 170 175  
Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn Phe  
180 185 190  
Glu Val Pro Phe Leu Thr Val Tyr Thr Gln Ala Ala Asn Leu His Leu  
195 200 205  
Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp Ser  
210 215 220  
Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr Ala  
225 230 235 240  
Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala Lys  
245 250 255  
Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe Arg  
260 265 270  
Arg Glu Met Thr Leu Thr Val Leu Asp Val Val Ala Leu Phe Pro Asn  
275 280 285  
Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr Arg  
290 295 300  
Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile Gly  
305 310 315 320  
Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser Val  
325 330 335  
Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val Tyr  
340 345 350  
Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp Ala  
355 360 365  
Gly His Gln Ile Ser Tyr His Arg Ile Phe Ser Asp Asn Ile Ile Lys  
370 375 380  
Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe Asp  
385 390 395 400  
Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val Leu  
405 410 415  
Leu Asp Ile Val Phe Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met Pro  
420 425 430  
Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys Thr  
435 440 445  
Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Gly Thr Arg Asp  
450 455 460  
Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr Glu



aaa ata gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga	291
Lys Ile Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly	
80 85 90	
tta ggt aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa	339
Leu Gly Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu	
95 100 105 110	
gaa aat cca aat ggt tca aga gcc tta cga gat gtg cga aat cga ttt	387
Glu Asn Pro Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe	
115 120 125	
gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg	435
Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val	
130 135 140	
aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac	483
Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn	
145 150 155	
ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg	531
Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp	
160 165 170	
gga tgg tca aca act act att aat aac tat tat gat cgt caa atg aaa	579
Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys	
175 180 185 190	
ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt	627
Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly	
195 200 205	
tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac	675
Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn	
210 215 220	
caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta	723
Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu	
225 230 235	
ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca caa	771
Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln	
240 245 250	
cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct	819
Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser	
255 260 265 270	
tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa	867
Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu	
275 280 285	
tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga ctc	915
Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu	
290 295 300	
aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata aga	963
Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg	
305 310 315	
cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt	1011
His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser	
320 325 330	



aat ctt caa caa atg tat gga act aat caa aat cta cac agc act agt	1059
Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser	
335 340 345 350	
acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag gat	1107
Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp	
355 360 365	
gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt	1155
Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe	
370 375 380	
gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc	1203
Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr	
385 390 395	
aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt	1251
Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser	
400 405 410	
aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca	1299
Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro	
415 420 425 430	
aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att ccc	1347
Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro	
435 440 445	
gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca cat	1395
Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His	
450 455 460	
cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act caa	1443
Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln	
465 470 475	
att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta	1491
Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val	
480 485 490	
aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga agt	1539
Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser	
495 500 505 510	
act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta	1587
Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu	
515 520 525	
gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca	1635
Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala	
530 535 540	
gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa aca	1683
Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr	
545 550 555	
atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat	1731
Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp	
560 565 570	
gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa	1779
Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys	

575                      580                      585                      590

cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac 1827  
 His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr  
                     595                      600                      605

gtt gac cga atc gaa ttc atc cca gta gat taa 1860  
 Val Asp Arg Ile Glu Phe Ile Pro Val Asp \*  
                     610                      615

<210> 20  
 <211> 616  
 <212> PRT  
 <213> Bacillus thuringiensis (truncated)

<400> 20  
 Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu  
   1                    5                    10                    15  
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys  
                     20                    25                    30  
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu  
                     35                    40                    45  
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln  
                     50                    55                    60  
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile  
                     65                    70                    75                    80  
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly  
                     85                    90                    95  
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn  
                     100                    105                    110  
 Pro Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile  
                     115                    120                    125  
 Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn  
                     130                    135                    140  
 Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His  
                     145                    150                    155                    160  
 Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp  
                     165                    170                    175  
 Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr  
                     180                    185                    190  
 Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala  
                     195                    200                    205  
 Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe  
                     210                    215                    220  
 Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro  
                     225                    230                    235                    240  
 Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr  
                     245                    250                    255  
 Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile  
                     260                    265                    270  
 Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser  
                     275                    280                    285  
 Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val  
                     290                    295                    300  
 Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp  
                     305                    310                    315                    320  
 Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu  
                     325                    330                    335  
 Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe  
                     340                    345                    350  
 Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val  
                     355                    360                    365

```

Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met
 370          375          380
Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys
385          390          395          400
Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg
          405          410          415
Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr
          420          425          430
Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr
          435          440          445
Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser
          450          455          460
Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro
465          470          475          480
Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly
          485          490          495
Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly
          500          505          510
Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys
          515          520          525
Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile
          530          535          540
Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn
545          550          555          560
Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile
          565          570          575
Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn
          580          585          590
Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp
          595          600          605
Arg Ile Glu Phe Ile Pro Val Asp
          610          615

```

<210> 21  
 <211> 2022  
 <212> DNA  
 <213> Bacillus thuringiensis (mutated)

<220>  
 <221> CDS  
 <222> (1)...(2022)  
 <221> misc\_feature  
 <222> (0)...(0)  
 <223> LKMS.N1218-1

```

<400> 21
atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1          5          10          15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
          20          25          30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
          35          40          45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
          50          55          60

```

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
tta aaa atg tct aat ggt tca aga gcc tta cga gat gtg cga aat cga	528
Leu Lys Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggg tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	

305	310	315	320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata				1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	325	330	335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga				1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	340	345	350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata				1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	355	360	365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt				1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	370	375	380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act				1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	385	390	395	400
agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag				1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	405	410	415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt				1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	420	425	430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat				1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	435	440	445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg				1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	450	455	460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa				1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	465	470	475	480
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att				1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	485	490	495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca				1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	500	505	510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act				1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	515	520	525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg				1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	530	535	540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga				1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	545	550	555	560
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca				1728

Ser Thr Gly	Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
	565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776	
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp		
	580 585 590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824	
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys		
	595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872	
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala		
	610 615 620	
gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg	1920	
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu		
	625 630 635 640	
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968	
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val		
	645 650 655	
tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg	2016	
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala		
	660 665 670	
gaa taa	2022	
Glu *		

<210> 22  
 <211> 673  
 <212> PRT  
 <213> Bacillus thuringiensis (mutated)

<400> 22

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
Leu Lys Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	



<210> 23  
 <211> 2013  
 <212> DNA  
 <213> Bacillus thuringiensis (mutated)

<220>  
 <221> CDS  
 <222> (1)...(2013)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> LKMS.R1218-1

<400> 23  
 atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48  
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
 1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192  
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
 50 55 60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240  
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
 65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288  
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
 85 90 95

act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336  
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp  
 100 105 110

gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384  
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
 115 120 125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432  
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn  
 130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca 480  
 Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro  
 145 150 155 160

tta aaa atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa atc 528  
 Leu Lys Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile  
 165 170 175

ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca aat 576  
 Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn  
 180 185 190

ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt cat 624



Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	Asn	Leu	His	
		195					200						205			
tta	ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	gaa	gaa	tgg	gga	tgg	672
Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	Trp	
	210					215				220						
tca	aca	act	act	att	aat	aac	tat	tat	gat	cgt	caa	atg	aaa	ctt	act	720
Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	Thr	
	225				230				235					240		
gca	gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	gaa	act	ggg	tta	gca	768
Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	Ala	
				245					250					255		
aaa	tta	aaa	ggc	acg	agc	gct	aaa	caa	tgg	gtt	gac	tat	aac	caa	ttc	816
Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	Phe	
			260					265					270			
cgt	aga	gaa	atg	aca	ctg	gcg	gtt	tta	gat	gtt	gtt	gca	tta	ttc	cca	864
Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	Pro	
		275					280					285				
aat	tat	gac	aca	cgc	acg	tac	cca	atg	gaa	acg	aaa	gca	caa	cta	aca	912
Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	Thr	
	290					295					300					
agg	gaa	gta	tat	aca	gat	cca	ctg	ggc	gcg	gta	aac	gtg	tct	tca	att	960
Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	Ile	
	305				310					315				320		
ggg	tcc	tgg	tat	gac	aaa	gca	cct	tct	ttc	gga	gtg	ata	gaa	tca	tcc	1008
Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	Ser	
				325					330					335		
gtt	att	cga	cca	ccc	cat	gta	ttt	gat	tat	ata	acg	gga	ctc	aca	gtg	1056
Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	Val	
			340					345					350			
tat	aca	caa	tca	aga	agc	att	tct	tcc	gct	cgc	tat	ata	aga	cat	tgg	1104
Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	Trp	
		355					360					365				
gct	ggg	cat	caa	ata	agc	tac	cat	cgt	gtc	agt	agg	ggg	agt	aat	ctt	1152
Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	Ser	Asn	Leu	
	370					375					380					
caa	caa	atg	tat	gga	act	aat	caa	aat	cta	cac	agc	act	agt	acc	ttt	1200
Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	Phe	
	385				390					395					400	
gat	ttt	acg	aat	tat	gat	att	tac	aag	act	cta	tca	aag	gat	gca	gta	1248
Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	Val	
				405					410					415		
ctc	ctt	gat	att	gtt	tac	cct	ggg	tat	acg	tat	ata	ttt	ttt	gga	atg	1296
Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	Met	
			420					425					430			
cca	gaa	gtc	gag	ttt	ttc	atg	gta	aac	caa	ttg	aat	aat	acc	aga	aag	1344
Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	Lys	
		435					440					445				

acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca aga	1392
Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg	
450 455 460	
gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat tat	1440
Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr	
465 470 475 480	
gag tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg	1488
Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr	
485 490 495	
ggg aac act acc gga tta gta cct gta ttt tct tgg aca cat cga agt	1536
Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser	
500 505 510	
gca gat tta aac aat aca ata tat tca gat aaa atc act caa att ccg	1584
Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro	
515 520 525	
gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa gga	1632
Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly	
530 535 540	
cca gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt	1680
Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly	
545 550 555 560	
tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa aaa	1728
Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys	
565 570 575	
gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat att	1776
Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp.Ile	
580 585 590	
gta ttg cat gta aac gat gct cag att cag atg cca aaa aca atg aac	1824
Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn	
595 600 605	
cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc	1872
Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile	
610 615 620	
aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat	1920
Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn	
625 630 635 640	
tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac	1968
Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp	
645 650 655	
cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg gaa taa	2013
Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu *	
660 665 670	

<210> 24  
 <211> 670  
 <212> PRT  
 <213> Bacillus thuringiensis (mutated)

&lt;400&gt; 24

```

Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro
 1          5          10          15
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu
 20          25          30
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met
 35          40          45
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val
 50          55          60
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu
 65          70          75          80
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr
 85          90          95
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp
100          105          110
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala
115          120          125
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn
130          135          140
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro
145          150          155          160
Leu Lys Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile
165          170          175
Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn
180          185          190
Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His
195          200          205
Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp
210          215          220
Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr
225          230          235          240
Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala
245          250          255
Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe
260          265          270
Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro
275          280          285
Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr
290          295          300
Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile
305          310          315          320
Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser
325          330          335
Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val
340          345          350
Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp
355          360          365
Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu
370          375          380
Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe
385          390          395          400
Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val
405          410          415
Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met
420          425          430
Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys
435          440          445
Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg
450          455          460
Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr
465          470          475          480
Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr
485          490          495

```

Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser  
                   500                  505                  510  
 Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro  
                   515                  520                  525  
 Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly  
                   530                  535                  540  
 Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly  
 545                  550                  555                  560  
 Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys  
                   565                  570                  575  
 Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile  
                   580                  585                  590  
 Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn  
                   595                  600                  605  
 Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile  
 610                  615                  620  
 Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn  
 625                  630                  635                  640  
 Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp  
                   645                  650                  655  
 Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu  
                   660                  665                  670

<210> 25  
 <211> 12  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> LKMS Insert

<400> 25  
 tta aaa atg tct

12

<210> 26  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> LKMS Insert

<400> 26  
 Leu Lys Met Ser  
 1

<210> 27  
 <211> 4874  
 <212> DNA  
 <213> *Bacillus thuringiensis*

<220>

<221> misc\_feature

<222> (0)...(0)

<223> Genomic DNA 1218-1

<400> 27  
 gggtttccatt cccaccggtt ttcactttca aaaaccccaa tacaccgaaa cttgtctatg 60  
 atgtgagtca tttatcttat ggcaaaagag atgtgtaaac gaacgattga cgtagaggat 120  
 tgtgggcaaa ttgagataga tttacatgtc ttaaaaatta aagggtgttt accgtttatc 180

gtgaacgtat	ccattgaacc	gcttagtatg	gaacatgtat	ataccacaag	tggttagagac	240
acatccttat	ttttaagttg	tcaagaaacg	gtatatgtgg	atcatatttt	aaaatatagt	300
gttgatcatg	tcccatatta	tgtaatgtat	ggccatcata	ttcaagtgcg	tgatgtatcg	360
attaaattga	tgaagaaaa	cccacaaact	gctcaaatat	cgggtgtttt	ttattttgat	420
tatgcataat	tataaaaaat	caaaaaatat	tttgtgaaga	atccctaaaa	ttatcacaac	480
attgtttatt	tataaataac	tcatttcaag	aaaaatcgta	atattttttt	atctaacagg	540
aattttatca	tctacagaag	aatattctta	tcattggtat	gaggagggag	agtgcacagag	600
aggggataga	caatcaaaa	agtatctaga	agagtttgtc	atgtaagaac	aaaaggaatc	660
tatcgtatat	gctactcaaa	agaaagtgtg	aaaaatcttt	gtatcttgta	tatgtatagg	720
aggaaaatag	atgagtccaa	ataatcaaaa	tgaatatgaa	attatagatg	cgacaccttc	780
tacttctgta	tccaatgatt	ctaacagata	ccctttttcg	aatgagccaa	caaatgcgct	840
acaaaaatag	gattataaag	attattttaa	aatgtctcgc	ggaaatgcta	gtgaataccc	900
tggttcacct	gaagtacttg	ttagcggaca	agatgcagct	aaggccgcaa	ttgatatagt	960
aggtaaatta	ctatcagggt	taggggtccc	atttgttggg	ccgatagtga	gtcttttatac	1020
tcaacttatt	gatattctgt	ggccttcagg	ggaaaagagt	caatgggaaa	tttttatgga	1080
acaagtagaa	gaactcatta	atcaaaaaat	agcagaatat	gcaaggaata	aagcgctttc	1140
ggaattagaa	ggatttaggt	ataattacca	attatatcta	actgcgcttg	aagaatggga	1200
agaaaaatcca	aatgggtcaa	gagccttacg	agatgtgcga	aatcgatttg	aaatcctgga	1260
tagtttattt	acgcaatata	tgccatcttt	tagagtgcga	aattttgaag	taccattcct	1320
tactgtatat	gcaatggcag	ccaaccttca	tttactgtta	ttaaaggacg	cgtcaatttt	1380
tggaagaaga	tggggatggg	caacaactac	tattaataac	tattatgatc	gtcaaatgaa	1440
acttactgca	gaatattctg	atcactgtgt	aaagtgggtg	gaaactgggt	tagcaaaaatt	1500
aaaaggcagc	agcgctaaac	aatgggttga	ctataaccaa	ttccgtagag	aaatgacact	1560
ggcggtttta	gagtgttttg	cattattccc	aaattatgac	acacgcacgt	acccaatgga	1620
aacgaagaca	caactaacaa	gggaagtata	tacagatcca	ctgggcgcgg	taaacgtgtc	1680
ttcaattggg	tcctgggtatg	acaaagcacc	ttctttcgga	gtgatagaat	catccgttat	1740
tcgaccaccc	catgtatttg	attatataac	gggactcaca	gtgtatacac	aatcaagaag	1800
catttcttcc	gctcgtcata	taagacattg	ggctgggtcat	caaataagct	accatcgtgt	1860
cagtaggggg	agtaactctc	aacaaatgta	tggaaactaat	caaatcttac	acagcactag	1920
tacctttgat	tttacgaatt	atgatattta	caagactcta	tcaaaggatg	cagtactcct	1980
tgatattggt	taccctgggt	atcgtatat	attttttgga	atgccagaag	tcgagttttt	2040
catggtaaac	caattgaata	ataccagaaa	gacgttaaag	tataatccag	tttccaaaga	2100
tattatagcg	agtacaagag	attcgggaatt	agaattacct	ccagaaactt	cagatcaacc	2160
aaattatgag	tcatatagcc	atagattatg	tcatatcaca	agtattcccg	cgacgggtaa	2220
cactaccgga	ttagtacctg	tattttcttg	gacacatcga	agtgcagatt	taaacaatac	2280
aatatattca	gataaaatca	ctcaaatccc	ggcgtttaa	tggtgggata	atttaccgtt	2340
tgttccagtg	gtaaaaggac	caggacatac	aggaggggat	ttattacagt	ataatagaag	2400
tactggttct	gtaggaacct	tatttctagc	tcgatatggc	ctagcattag	aaaaagcagg	2460
gaaatatcgt	gtaagactga	gatatgctac	tgatgcagat	attgtattgc	atgtaaacga	2520
tgctcagatt	cagatgccaa	aaacaatgaa	cccagggtgag	gatctgacat	ctaaaacttt	2580
taaagtgtga	gatgtatca	caacattaaa	tttagcaaca	gatagttcgc	tagcattgaa	2640
acataattta	gggtgaagacc	ctaattcaac	attatctggg	atagtttacg	ttgaccgaat	2700
cgaattcatc	ccagtagatg	agacatatga	agcggaaaca	gatttagaag	cagcgaagaa	2760
agcagtgaat	gccttggtta	cgaatacaaa	agatggctta	cgaccaggcg	taacggatta	2820
tgaagtgaat	caagcggcaa	acttagtgga	atgcctatcg	gatgatttgt	atccaaatga	2880
aaaacgattg	ttatttgatg	cagtgcagga	ggcaaaacgc	ctcagtgcag	cacgtaattt	2940
gcttcaagat	ccagatttcc	aagagataaa	tgagaaaaat	ggctggacgg	caagtacggg	3000
aattgagggt	atgcatttatt	caaaggcggt	tatctacgcc	taccaggtgc	taccaggtgc	3060
gagagaaata	gatacggaaa	cgtatccaac	gtatctgtat	caaaaagtag	aggaagggtg	3120
attaaaacca	tacacaagat	atagattgag	agggtttgtc	ggaagcagtc	aaggattgga	3180
aattttcaca	attcgtcatc	aaacgaaccg	aattgtaaaa	aatgtaccgg	atgatttgct	3240
gccagatgta	tctcctgtta	actcggatgg	tagtatcaat	cgatgcagcg	aacaaaagta	3300
tgtgaataga	cgtttagaag	tagaaaaaccg	ttctgggtgaa	gcgcagtagt	tctctattcc	3360
tattgataca	gggtgaatcg	attacaatga	aaatgcagga	atatgggttg	gatttaagat	3420
tacggacca	gagggatatg	caacactcgg	aaacctagaa	ttggtcgaag	agggaccttt	3480
atcaggagac	gcattagaac	gcttgcaaa	agaagaacaa	cagtgggaaga	ttcaaatgac	3540
aagaagacgt	gaagaaacag	atagaaggta	tatggcatcg	aaacaagcgg	tagatcgttt	3600
atatgccgat	tatcaggatc	agcaactgaa	tcctgatgta	gagattacag	atcttactgc	3660
ggcccaagat	ctgatacagt	ccattcctta	cgtatataac	gaaatgttcc	cagaaatacc	3720
agggatgaac	tatacgaagt	ttacagaatt	aacagatcga	ctccaacaag	cgtggagtgt	3780
gtatgatcag	cgaaatgcc	taccaaatgg	tgattttcga	aatgggttaa	gtaattggaa	3840
tgcaacgcct	ggcgtagaag	tacaacaaat	caatcataca	tctgtccttg	tgattccaaa	3900
ctgggatgag	caagtttcgc	aacagtttac	agttcaaccg	aatcaaagat	atgtgttacg	3960

```

agttactgcg agaaaagaag gggtaggaaa tggatatgta agtatccgtg atggtggaaa 4020
tcaaacagaa acgcttactt ttagtgcaag cgattatgat acaaatggaa tgtataatac 4080
gcaagtgtcc aatacaaatg gatataacac aaataatgcg tataatacac aagcatcgag 4140
tacaacgga tataacgcaa ataatatgta taatacgcaa gcatcgaata caaacggata 4200
taacacaaat agtgtgtaca atgatcaaac cggctatata acaaaaacag tgacattcat 4260
cccgatatata gatcaaatgt ggattgagat gagtgagaca gaaggtagat tctatataga 4320
aagtgtagaa ttgattgtag acgtagagta atagtagtac ccctccagat gaaacctgta 4380
tctggagggg ttttttatgc aaaagagtct tttcatacag aatatattgg ttttaccggg 4440
attacatatt ttgtgaatag gactatgggt ggttacctta cggtagcttt ttatatccac 4500
cggcattgga aaatgtaaga gggaggataa tcatatatag tcccttccct acacatcaaa 4560
ttccttcgaa agtttctcgt gaatgagagt gaatatttct ttttgtactt tattcaggtc 4620
ttgttaagaaa ggaatggtat tcacacaaat gatgggtgtg gatacgtctg ttaaaccctga 4680
gatattttgta ataatacaagt catagttttt tgcaatctgt ttaaatgagc tgagatgtaa 4740
tacatcaatc ttagatagtt gaatcatatg accaaattga tactgcataa tattacgaat 4800
aaatagggtg tgttccatat ctgaatcaca aaaaatgccg acatgaagaa caggaacctt 4860
ctgttttaaa gctt 4874

```

```

<210> 28
<211> 6613
<212> DNA
<213> Bacillus thuringiensis

```

```

<220>
<221> misc_feature
<222> (0)...(0)
<223> Genomic Cry12I8-2

```

```

<400> 28
tttttaggtat tcttttaagt tctttataga gacagattaa cgaaaaacta aataagaaat 60
tcaatccctt gatacatgat gcatcggatg ccaaattatt agtacgtatc ttgcgtatat 120
tgtacgaggt cgaattgacg taacagggca ccttttttgt caaattgacc aaagaatcca 180
tcctttgcat gagcacttct cgaaaccact tcccatagtg cacttcttat cttttgtata 240
tatttcctaa ggatatacgt atccctattt ctgataagag gatattgtca gtgtaggaag 300
agcgaatgtc ttttcgtatt tcaaacaaaa aataaaggat gtttatgcac ggaaataatc 360
atcatattaa taatgccagc tacataaaga tagatggggg tcattttttg aaatgattcg 420
aaaaagactcc gttgactcga taggaggtgc acagaaaaat ggaagaaaga tatgcatcgc 480
aagatcagtc ggtagttaga gtttctaata gcaaggggaa gaaaaaccat acagttccct 540
ttcaatgtat ggtttccatt ccaacagggt ttcaaattca aaaacccaat acaccgaaac 600
ttgtctatga tgtgagtcac ttatctatgg caaaagagat gtgtaaacga acgattgacg 660
tagaggattg tgggcaaatg gagatagatt tacatgtcct aaaaattaaa ggtgttttac 720
cgtttatcgt gaacgtatcc attgaaccgc ttagtatgaa catgtatata ccacaagtgg 780
tagagacaca tccttatttt taagtgtgca agaaacggtg tatgtggatc atatttttaa 840
atatagtggt cgtattatgc cgtattatgt aattgatggc catcatattc aagtgcgtga 900
tgtatcgatt aaattgatgg aagaaaacc ccaaaactgct caaatatcgg gtgtttttta 960
ttttgattat gcataatttt aaaaaatcaa aaaatatatt gtgaagaatc cctaaaatta 1020
tcacaacatt gtttattata aaataactca tttcaagaaa aatcgtaata tttttttatc 1080
taacaggaat tttatcatct acagaagaat attccttatca tggtaatgag gaggagagat 1140
gacagtcaaa agagtacctg gtttgtcgtg taagaaaaaa gaatcgatcg tacaggaaa 1200
ttaaaaaaaag tgtaagaaat tttatatcct ttgtatgtat aggaggaaaa tagatgagtc 1260
caaataatca aaatgaatat gaaattatag atgcgacacc ttctacttct gtatccaatg 1320
attctaacag ataccctttt gcgaatgagc caacaaatgc gctacaaaat atggattata 1380
aagattattt aaaaatgtct gcgggaaatg ctagtgaata ccctgggttca cctgaagtac 1440
ttgttagcgg acaagatgca gctaaggccg caattgatat agtaggtaaa ttactatcag 1500
gttttaggggt cccattttgtt gggccgatag tgagtcttta tactcaactt attgatattc 1560
tgtggcccttc agggcaaaaag agtcaatggg agatttttat ggaacaagta gaagaactca 1620
taaatcaaaa aatagcagaa tatgcaagga ataaagcgct ttcggaatta gaaggattag 1680
gtaataatta ccaattatat ctaactgcgc ttgaagaatg gaaagaaaat ccaaatgggt 1740
caagagcctt acgagatgtg cgaaatcgat ttgaaatcct ggatagttta tttacgcaat 1800
acatgccatc ttttcgagtg acaaattttg aagtaccatt ccttacagta tatacacagg 1860
cagccaacct tcattttactg ttattaaagg acgcttcaat ttttggagaa gaatggggat 1920
ggctacaac cactattaat aactattatg atcgtcaaat gaaacttact gcagaatatt 1980
ctgatcactg tgtaaagtgg tatgaaactg gtttagcaaa attaaaaggc acgagcgcta 2040
aacaatgggt cgactataac caattccgta gagaaatgac actgacggtt ttagatgttg 2100

```

ttgcattatt	cccaaattat	gacacacgca	cgtacccaat	ggaaacgaaa	gcacaactaa	2160
caagggaagt	atatacagat	ccactgggcg	cggtaaactg	gtcttcaatt	ggttcctggt	2220
atgacaaagc	accttctttc	ggagtgtatg	aatcatccgt	tattcgacca	ccccatgtat	2280
ttgattatat	aacgggactc	acagtgtata	cacaatcaag	aagcatttct	tccgctcgct	2340
atataagaca	ttgggctggt	catcaaataa	gctatcatcg	gatttttagt	gataatatta	2400
taaaacagat	gtatggaact	aatcaaaatc	tacacagcac	tagtaccttt	gattttacga	2460
attatgatat	ttacaagacg	ttatcaaaag	atgcggtgct	ccttgatatt	gtttttcctg	2520
gttatacgtg	tatatTTTTT	ggaatgccag	aagtcgagtt	tttcatggta	aaccaattga	2580
ataataccag	aaagacgtta	aagtataatc	cggtttccaa	agatattata	gcggggacaa	2640
gagattcgga	attagaatta	cctccagaaa	cttcagatca	accaaattat	gagtcataata	2700
gccatagatt	atgtcatatc	acaagtattc	ccgcgacggg	ttcaactacc	ggattagtag	2760
ctgtattttc	ttggacacat	cggagtgcgg	atcttataaa	tgcagttcat	tcagataaaa	2820
ttactcagat	tccggtcgta	aaggtttctg	atttggtctc	ctctataaca	ggagggccaa	2880
ataataccgt	tgtatcgggt	cctggattta	cagggggggg	gataataaaa	gtaataagaa	2940
atggagtaat	tatatcacat	atgcgtgtta	aaatttcaga	cattaacaaa	gaatatagta	3000
tgaggattcg	gtatgcttcc	gctaataata	ctgaatttta	tataaatcct	tctgaagaaa	3060
acgltaaatc	tcacgctcaa	aaaactatga	atagaggtga	agctttaaca	tataataaat	3120
ttaatttatg	gactttgccc	cctattaaat	ttacgacaac	cgaacctttc	attactctag	3180
gggctatatt	tgaagcggaa	gactttcttg	gaattgaagc	ttatatagac	cgaatcgaat	3240
ttatcccagt	agatgagaca	tatgaagcgg	aacaagattt	agaagcagcg	aagaaagcag	3300
tgaatgcctt	gtttacgaat	acaaaagatg	gcttacgacc	aggcgtaacg	gattatgaag	3360
tgaatcaagc	ggcaaactta	gtggaatgcc	tatcggtatg	tttgtatcca	aatgaaaaac	3420
gattgttatt	tgatgcatg	agagaggcaa	aacgcctcag	tgaggcacgt	aatttgcttc	3480
aagatccaga	ttccaagag	ataaatggag	aaaatggctg	gacggcaagt	acgggaattg	3540
aggttataga	aggggatgct	ttattcaaa	ggcggttatc	acgcctacca	ggtgcgagag	3600
aaatagatac	ggaaacgtat	ccaacgtatc	tgtatcaaaa	agtagaggaa	ggtgtattaa	3660
aaccatacac	aagatataga	ttgagagggg	ttgtcggaa	cagtcaggga	ttggaaattt	3720
tcacaattcg	tcatacaacg	aaccgaattg	taaaaaatgt	accggatgat	ttgctgccag	3780
atgtatctcc	tgtaactc	gatggtatga	tcaatcgatg	cagcgaacaa	aagtatgtga	3840
atagccgttt	agaagttaga	aaccgttctg	gtgaagcgca	tgagtctctc	attcctattg	3900
atacaggtga	aatcgattac	aatgaaaatg	caggaatatg	ggttggattt	aagattacgg	3960
accagagggg	atatgcaaca	ctcggaaacc	tagaattggt	cgaagaggga	cctttatcag	4020
gagacgcatt	agaacgcttg	caaagagaag	aacaacagtg	gaagattcaa	atgacaagaa	4080
gacgtgaaga	aacagataga	aggtatatgg	catcgaaaca	agcggtagat	cgttttatatg	4140
ccgattatca	ggatcagcaa	ctgaatcctg	atgtagagat	tacagatctt	actgcggccc	4200
aagatctgat	acagtcctat	ccttacgtat	ataacgaaat	gttcccagaa	ataccaggga	4260
tgaactatac	gaagtttaca	gaatttaacag	atcgactcca	acaagcgtgg	agtttgtatg	4320
atcagcga	tgccatacca	aatggtgatt	ttcgaaatgg	gttaagtaat	tggaaatgcaa	4380
cgctggcg	agaagtacaa	caaatacaatc	atacatctgt	ccttggtgatt	ccaaactggg	4440
atgagcaagt	ttcgcaacag	tttacagttc	aaccgaatca	aagatatgtg	ttacgagtta	4500
ctgcgagaaa	agaaggggta	ggaaatggat	atgtaagtat	ccgtgatggt	ggaaatcaaa	4560
cagaaacgct	tacttttagt	gcaagcgatt	atgatacaaa	tggaaatgtat	aatacgcaag	4620
tgtccaat	aaatggatat	aacacaaaata	atgcgtataa	tacacaagca	tcgagtacaa	4680
acggatataa	cgcaataaat	atgtataata	cgcaagcatc	gaatacaaac	ggatataaca	4740
caaatagtgt	gtacaatgat	caaaccggct	atatcacaaa	aacagtga	ttcatcccgt	4800
atacagatca	aatgtggatt	gagatgagtg	agacagaagg	tacattctat	atagaaagtg	4860
tagaattgat	tgtagacgta	gagtaatagt	agtacccctc	cagatgaaac	ctgtatctgg	4920
aggggttttt	tatgcaaaa	agtcttttca	tacagaatat	attggtttta	cccggattac	4980
atattttgtg	aataggacta	tggttggtta	ccttacggta	cctttttata	tccaccggca	5040
ttggaaaatg	taagaggggag	gataatcata	tatagtccct	tccctacaca	tcaaattcct	5100
tcgaaagt	ctcgtgaatg	agagtgaata	tttctttttg	tactttattc	aggtcttgta	5160
agaaaggaat	ggtattcaca	caaatagatg	gtgtggatag	gtctgttaaa	cctgagatat	5220
ttgtaataat	caagtcatag	ttttttgcaa	tctgttttaa	tgagctgaga	tgtaatacat	5280
caatcttaga	tagttgaatc	atatgaccaa	attgatactg	cataatatta	cgaataaata	5340
gggtatgttc	catatctgaa	tcacaaaaaa	tgccgacatg	aagaacagga	accttctgtt	5400
ttaaagcttg	taataagttt	gtccaatgta	tgattaaaat	atataatggt	tccgtaaaaa	5460
catgctcgtc	ccatttgaac	tgttcatgat	agtgaagtgt	agttaattct	tcttttaaaa	5520
gcaagacaaa	gtatgaaaat	tcgtgagaat	gatgctcgga	aaaaaacgt	cttttatcat	5580
gtaaaaataa	actacgtcca	taattcatgg	tttgtaaat	gtataactcc	aaaatgattt	5640
tttgtttatt	ttggagaggc	acatgtagtt	tgtcggatag	tctatgcaat	aagtttagaa	5700
tttcaggaa	aattttccat	gcgtcatttg	atttttgttg	taccatagtt	tctaattgct	5760
catacgtaaa	tgcataatga	tgattaaaaa	aaacagagaa	gagttggtaa	acagtcctcat	5820
gattaaaatc	aagagaaaag	gtatcccgga	acaattgaca	aaatgagctg	ttctcaaaaa	5880

```

tacttacatc caaaggattg gaaaaatctt ctgaaatggg tttcatatgc tgggtgttgta 5940
aacgaatcac attcaccatt gtccaatacc gaatccgtat gaggtctgga aaatttagtt 6000
gtatctgatt tttttgggtg acatatagaa agagttgatc caatgcctgt agttgggtgt 6060
ctgggaaagg agtatgagtc acaccatatt tttcataaaa aaactggacc ataatacttc 6120
taatatgttg ttcatttcct atgattttac aaggatttgt ttgaatgtgt atctcatatt 6180
gttcgagata cacattcaat tttgtgataa tccgccttag ggtggaagta ctaagaaata 6240
attcctccgc gattgtctct atgtcatctc tttcatcaaa aaatatccgt tcgataaagg 6300
aaaactcagg acttacagat aagacctttt gatataataa atcaatagaa tactgagaag 6360
gataggttaa cataatccct tttatagatg tctcaatctg aaaaggttga aattccttgat 6420
taataaattt aatgtcatct ctcaaaattc tttcggaaca atttagtgtt tgtgcactca 6480
ctcctaacgt atgccatcca tcttgttcat atagtgttc taagaattgt agttgtctgc 6540
gtaaattggt atttaaaaga gaacgcatga gtagacacct tctttcattt ataaaatatac 6600
actgatggaa ttc 6613

```

```

<210> 29
<211> 1863
<212> DNA
<213> Bacillus thuringiensis (mutated)

```

```

<220>
<221> CDS
<222> (1)...(1863)

<221> misc_feature
<222> (0)...(0)
<223> NGS.R.N49FVD

```

```

<400> 29
atg tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt 48
Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu
1 5 10 15

ggt agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa 96
Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
20 25 30

tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt 144
Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
35 40 45

tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa 192
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
50 55 60

tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata 240
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
65 70 75 80

gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt 288
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
85 90 95

aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat 336
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
100 105 110

cca aat ggt tca aga aat ggt tcc cgg gcc tta cga gat gtg cga aat 384
Pro Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn
115 120 125

cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt 432

```



Arg	Phe	Glu	Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe		
130						135					140						
aga	gtg	aca	aat	ttt	gaa	gta	cca	ttc	ctt	act	gta	tat	gca	atg	gca	480	
Arg	Val	Thr	Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala		
145					150					155					160		
gcc	aac	ctt	cat	tta	ctg	tta	tta	aag	gac	gcg	tca	att	ttt	gga	gaa	528	
Ala	Asn	Leu	His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu		
				165					170					175			
gaa	tgg	gga	tgg	tca	aca	act	act	att	aat	aac	tat	tat	gat	cgt	caa	576	
Glu	Trp	Gly	Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln		
			180					185					190				
atg	aaa	ctt	act	gca	gaa	tat	tct	gat	cac	tgt	gta	aag	tgg	tat	gaa	624	
Met	Lys	Leu	Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu		
			195				200					205					
act	ggt	tta	gca	aaa	tta	aaa	ggc	acg	agc	gct	aaa	caa	tgg	gtt	gac	672	
Thr	Gly	Leu	Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp		
	210					215				220							
tat	aac	caa	ttc	cgt	aga	gaa	atg	aca	ctg	gcg	gtt	tta	gat	gtt	gtt	720	
Tyr	Asn	Gln	Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val		
	225				230					235					240		
gca	tta	ttc	cca	aat	tat	gac	aca	cg	acg	tac	cca	atg	gaa	acg	aaa	768	
Ala	Leu	Phe	Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys		
				245					250					255			
gca	caa	cta	aca	agg	gaa	gta	tat	aca	gat	cca	ctg	ggc	g	gta	aac	816	
Ala	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn		
			260					265					270				
gtg	tct	tca	att	ggt	tcc	tgg	tat	gac	aaa	gca	cct	tct	ttc	gga	gtg	864	
Val	Ser	Ser	Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val		
			275				280					285					
ata	gaa	tca	tcc	gtt	att	cga	cca	ccc	cat	gta	ttt	gat	tat	ata	acg	912	
Ile	Glu	Ser	Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr		
	290					295				300							
gga	ctc	aca	gtg	tat	aca	caa	tca	aga	agc	att	tct	tcc	gct	cg	tat	960	
Gly	Leu	Thr	Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr		
	305				310				315					320			
ata	aga	cat	tgg	gct	ggt	cat	caa	ata	agc	tac	cat	cgt	gtc	agt	agg	1008	
Ile	Arg	His	Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg		
				325					330					335			
ggt	agt	aat	ctt	caa	caa	atg	tat	gga	act	aat	caa	aat	cta	cac	agc	1056	
Gly	Ser	Asn	Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser		
			340					345					350				
act	agt	acc	ttt	gat	ttt	acg	aat	tat	gat	att	tac	aag	act	cta	tca	1104	
Thr	Ser	Thr	Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser		
			355				360					365					
aag	gat	gca	gta	ctc	ctt	gat	att	gtt	tac	cct	ggt	tat	acg	tat	ata	1152	
Lys	Asp	Ala	Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile		
	370					375					380						



<212> PRT  
 <213> Bacillus thuringiensis (mutated)

<400> 30

```

Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu
 1          5          10          15
Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
          20          25          30
Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
 35          40          45
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
 50          55          60
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
 65          70          75          80
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
          85          90          95
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
 100          105          110
Pro Asn Gly Ser Arg Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn
 115          120          125
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe
 130          135          140
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala
 145          150          155          160
Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu
          165          170          175
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln
 180          185          190
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu
 195          200          205
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp
 210          215          220
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val
 225          230          235          240
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys
          245          250          255
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn
          260          265          270
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val
 275          280          285
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr
 290          295          300
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr
 305          310          315          320
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg
          325          330          335
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser
          340          345          350
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser
 355          360          365
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile
 370          375          380
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn
 385          390          395          400
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile
          405          410          415
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp
          420          425          430
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser
          435          440          445
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp
 450          455          460
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile

```

465                      470                      475                      480  
 Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro  
                                  485                      490                      495  
 Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn  
                                  500                      505                      510  
 Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu  
                                  515                      520                      525  
 Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr  
                                  530                      535                      540  
 Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro  
 545                      550                      555                      560  
 Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val  
                                  565                      570                      575  
 Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala  
                                  580                      585                      590  
 Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile  
                                  595                      600                      605  
 Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp  
                                  610                      615                      620

<210> 31  
 <211> 1863  
 <212> DNA  
 <213> Bacillus thuringiensis (mutated)

<220>  
 <221> CDS  
 <222> (1)...(1863)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> LKMS.N49PVD

<400> 31  
 atg tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt    48  
 Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu  
   1                                  5                                  10                                  15  
  
 gtt agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa    96  
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys  
                                   20                                  25                                  30  
  
 tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt    144  
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu  
                                   35                                  40                                  45  
  
 tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa    192  
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln  
                                   50                                  55                                  60  
  
 tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata    240  
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile  
                                   65                                  70                                  75                                  80  
  
 gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt    288  
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly  
                                   85                                  90                                  95  
  
 aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat    336  
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn  
                                   100                                  105                                  110

cca tta aaa atg tct aat ggt tct aga gcc tta cga gat gtg cga aat	384
Pro Leu Lys Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn	
115 120 125	
cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt	432
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe	
130 135 140	
aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca	480
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala	
145 150 155 160	
gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa	528
Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu	
165 170 175	
gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa	576
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln	
180 185 190	
atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa	624
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu	
195 200 205	
act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac	672
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp	
210 215 220	
tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt	720
Tyr Asn Gln Phe Arg Glu Met Thr Leu Ala Val Leu Asp Val Val	
225 230 235 240	
gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa	768
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys	
245 250 255	
gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac	816
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn	
260 265 270	
gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg	864
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val	
275 280 285	
ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg	912
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr	
290 295 300	
gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat	960
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr	
305 310 315 320	
ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg	1008
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg	
325 330 335	
ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc	1056
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser	
340 345 350	
act agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca	1104
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser	
355 360 365	

aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata	1152
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile	
370 375 380	
ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat	1200
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn	
385 390 395 400	
aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata	1248
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile	
405 410 415	
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat	1296
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp	
420 425 430	
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt	1344
Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser	
435 440 445	
att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg	1392
Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp	
450 455 460	
aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc	1440
Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile	
465 470 475 480	
act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca	1488
Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro	
485 490 495	
gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat	1536
Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn	
500 505 510	
aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta	1584
Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu	
515 520 525	
gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act	1632
Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr	
530 535 540	
gat gca gat att gta ttg cat gta aac gat gct cag att cag atg cca	1680
Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro	
545 550 555 560	
aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt	1728
Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val	
565 570 575	
gca gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca	1776
Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala	
580 585 590	
ttg aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata	1824
Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile	
595 600 605	
gtt tac gtt gac cga atc gaa ttc atc cca gta gat taa	1863
Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp *	

610

615

620

&lt;210&gt; 32

&lt;211&gt; 620

&lt;212&gt; PRT

<213> *Bacillus thuringiensis* (mutated)

&lt;400&gt; 32

```

Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu
 1           5           10           15
Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys
          20           25           30
Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu
          35           40           45
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln
          50           55           60
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile
          65           70           75           80
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly
          85           90           95
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn
          100          105          110
Pro Leu Lys Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn
          115          120          125
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe
          130          135          140
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala
          145          150          155          160
Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu
          165          170          175
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln
          180          185          190
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu
          195          200          205
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp
          210          215          220
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val
          225          230          235          240
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys
          245          250          255
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn
          260          265          270
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val
          275          280          285
Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr
          290          295          300
Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr
          305          310          315          320
Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg
          325          330          335
Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser
          340          345          350
Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser
          355          360          365
Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile
          370          375          380
Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn
          385          390          395          400
Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile
          405          410          415
Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp
          420          425          430

```

Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser  
 435 440 445  
 Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp  
 450 455 460  
 Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile  
 465 470 475 480  
 Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro  
 485 490 495  
 Val Val Lys Gly Pro Gly His Thr Gly Asp Leu Leu Gln Tyr Asn  
 500 505 510  
 Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu  
 515 520 525  
 Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr  
 530 535 540  
 Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro  
 545 550 555 560  
 Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val  
 565 570 575  
 Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala  
 580 585 590  
 Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile  
 595 600 605  
 Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp  
 610 615 620

<210> 33  
 <211> 1854  
 <212> DNA  
 <213> Bacillus thuringiensis (mutated)

<220>  
 <221> CDS  
 <222> (1)...(1854)  
 <221> misc\_feature  
 <222> (0)...(0)  
 <223> LKMS.R49PVD

<400> 33  
 atg tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt 48  
 Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu  
 1 5 10 15  
 gtt agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa 96  
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys  
 20 25 30  
 tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt 144  
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu  
 35 40 45  
 tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa 192  
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln  
 50 55 60  
 tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata 240  
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile  
 65 70 75 80  
 gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt 288  
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly  
 85 90 95



aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat	336
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn	
100 105 110	
cca tta aaa atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa	384
Pro Leu Lys Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu	
115 120 125	
atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca	432
Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr	
130 135 140	
aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt	480
Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu	
145 150 155 160	
cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga	528
His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly	
165 170 175	
tgg tca aca act act att aat aac tat tat gat cgt caa atg aaa ctt	576
Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu	
180 185 190	
act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta	624
Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu	
195 200 205	
gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa	672
Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln	
210 215 220	
ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc	720
Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe	
225 230 235 240	
cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta	768
Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu	
245 250 255	
aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca	816
Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser	
260 265 270	
att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca	864
Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser	
275 280 285	
tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca	912
Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr	
290 295 300	
gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata aga cat	960
Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His	
305 310 315 320	
tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt aat	1008
Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn	
325 330 335	
ctt caa caa atg tat gga act aat caa aat cta cac agc act agt acc	1056
Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr	

340	345	350	
ttt gat ttt acg aat tat gat att tac aag act cta tca aag gat gca			1104
Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala			
355	360	365	
gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga			1152
Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly			
370	375	380	
atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga			1200
Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg			
385	390	395	400
aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca			1248
Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr			
405	410	415	
aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat			1296
Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn			
420	425	430	
tat gag tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg			1344
Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala			
435	440	445	
acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca cat cga			1392
Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg			
450	455	460	
agt gca gat tta aac aat aca ata tat tca gat aaa atc act caa att			1440
Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile			
465	470	475	480
ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa			1488
Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys			
485	490	495	
gga cca gga cat aca gga ggg gat tta tta cag tat aat aga agt act			1536
Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr			
500	505	510	
ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa			1584
Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu			
515	520	525	
aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat			1632
Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp			
530	535	540	
att gta ttg cat gta aac gat gct cag att cag atg cca aaa aca atg			1680
Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met			
545	550	555	560
aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct			1728
Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala			
565	570	575	
atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat			1776
Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His			
580	585	590	
aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt			1824

Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val  
 595 600 605

gac cga atc gaa ttc atc cca gta gat taa  
 Asp Arg Ile Glu Phe Ile Pro Val Asp \*  
 610 615

1854

<210> 34  
 <211> 617  
 <212> PRT  
 <213> Bacillus thuringiensis (mutated)

<400> 34  
 Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu  
 1 5 10 15  
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ile Asp Ile Val Gly Lys  
 20 25 30  
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu  
 35 40 45  
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln  
 50 55 60  
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile  
 65 70 75 80  
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly  
 85 90 95  
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn  
 100 105 110  
 Pro Leu Lys Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu  
 115 120 125  
 Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr  
 130 135 140  
 Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu  
 145 150 155 160  
 His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly  
 165 170 175  
 Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu  
 180 185 190  
 Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu  
 195 200 205  
 Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln  
 210 215 220  
 Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe  
 225 230 235 240  
 Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu  
 245 250 255  
 Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser  
 260 265 270  
 Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser  
 275 280 285  
 Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr  
 290 295 300  
 Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His  
 305 310 315 320  
 Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn  
 325 330 335  
 Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr  
 340 345 350  
 Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala  
 355 360 365  
 Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly  
 370 375 380  
 Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg

385                      390                      395                      400  
 Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr  
                          405                      410                      415  
 Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn  
                          420                      425                      430  
 Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala  
                          435                      440                      445  
 Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg  
                          450                      455                      460  
 Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile  
 465                      470                      475                      480  
 Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys  
                          485                      490                      495  
 Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr  
                          500                      505                      510  
 Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu  
                          515                      520                      525  
 Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp  
 530                      535                      540  
 Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met  
 545                      550                      555                      560  
 Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala  
                          565                      570                      575  
 Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His  
                          580                      585                      590  
 Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val  
                          595                      600                      605  
 Asp Arg Ile Glu Phe Ile Pro Val Asp  
 610                      615

<210> 35  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 5' forward primer

<400> 35  
 atgagtccaa ataatacaaaa tg 22

<210> 36  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 5' reverse primer

<400> 36  
 ccgcttctaa atcttggtcc 20

<210> 37  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 3' forward primer

<400> 37  
 ggaacaagat ttagagg 17

<210> 38  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 3' reverse primer

<400> 38  
 ctcacgtct acaatcaatt catc 24

<210> 39  
 <211> 2022  
 <212> DNA  
 <213> Bacillus thuringiensis (mutated)

<220>  
 <221> CDS  
 <222> (1)...(2022)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> LRNS.N1218-1

<400> 39  
 atg agt cca aat aat caa aat gaa tat gaa att ata gat gcg aca cct 48  
 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
 1 5 10 15

tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag 96  
 Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
 20 25 30

cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg 144  
 Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
 35 40 45

tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt 192  
 Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
 50 55 60

agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta 240  
 Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
 65 70 75 80

cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat 288  
 Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
 85 90 95

act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg 336  
 Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp  
 100 105 110

gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca 384  
 Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
 115 120 125

gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat 432  
 Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn  
 130 135 140

aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca 480

Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
tta aga atg tct aat ggt tca aga gcc tta cga gat gtg cga aat cga	528
Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg	
165 170 175	
ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga	576
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg	
180 185 190	
gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc	624
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala	
195 200 205	
aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa	672
Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu	
210 215 220	
tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa atg	720
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met	
225 230 235 240	
aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act	768
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr	
245 250 255	
ggg tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat	816
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr	
260 265 270	
aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca	864
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala	
275 280 285	
tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca	912
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala	
290 295 300	
caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg	960
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val	
305 310 315 320	
tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata	1008
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile	
325 330 335	
gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga	1056
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly	
340 345 350	
ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata	1104
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile	
355 360 365	
aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt	1152
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly	
370 375 380	
agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc act	1200
Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr	
385 390 395 400	

agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca aag	1248
Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys	
405 410 415	
gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt	1296
Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe	
420 425 430	
ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat	1344
Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn	
435 440 445	
acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg	1392
Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala	
450 455 460	
agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa	1440
Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln	
465 470 475 480	
cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt att	1488
Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile	
485 490 495	
ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg aca	1536
Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr	
500 505 510	
cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc act	1584
His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr	
515 520 525	
caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg	1632
Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val	
530 535 540	
gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat aga	1680
Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg	
545 550 555 560	
agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta gca	1728
Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala	
565 570 575	
tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act gat	1776
Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp	
580 585 590	
gca gat att gta ttg cat gta aac gat gct cag att cag atg cca aaa	1824
Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys	
595 600 605	
aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca	1872
Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala	
610 615 620	
gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca ttg	1920
Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu	
625 630 635 640	
aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt	1968
Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val	
645 650 655	

tac gtt gac cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg 2016  
Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala  
660 665 670

gaa taa 2022  
Glu \*

<210> 40  
<211> 673  
<212> PRT  
<213> *Bacillus thuringiensis* (mutated)

<400> 40  
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro  
1 5 10 15  
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu  
20 25 30  
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met  
35 40 45  
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val  
50 55 60  
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu  
65 70 75 80  
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr  
85 90 95  
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp  
100 105 110  
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala  
115 120 125  
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn  
130 135 140  
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro  
145 150 155 160  
Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn Arg  
165 170 175  
Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg  
180 185 190  
Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala  
195 200 205  
Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu  
210 215 220  
Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met  
225 230 235 240  
Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr  
245 250 255  
Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr  
260 265 270  
Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala  
275 280 285  
Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala  
290 295 300  
Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val  
305 310 315 320  
Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile  
325 330 335  
Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly  
340 345 350  
Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile  
355 360 365  
Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly





tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt	144
Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu	
35 40 45	
tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa	192
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln	
50 55 60	
tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata	240
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Ile Asn Gln Lys Ile	
65 70 75 80	
gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt	288
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly	
85 90 95	
aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat	336
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn	
100 105 110	
cca tta aga atg tct aat ggt tcc cgg gcc tta cga gat gtg cga aat	384
Pro Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn	
115 120 125	
cga ttt gaa atc ctg gat agt tta ttt acg caa tat atg cca tct ttt	432
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe	
130 135 140	
aga gtg aca aat ttt gaa gta cca ttc ctt act gta tat gca atg gca	480
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala	
145 150 155 160	
gcc aac ctt cat tta ctg tta tta aag gac gcg tca att ttt gga gaa	528
Ala Asn Leu His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu	
165 170 175	
gaa tgg gga tgg tca aca act act att aat aac tat tat gat cgt caa	576
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln	
180 185 190	
atg aaa ctt act gca gaa tat tct gat cac tgt gta aag tgg tat gaa	624
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu	
195 200 205	
act ggt tta gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac	672
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp	
210 215 220	
tat aac caa ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt	720
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val	
225 230 235 240	
gca tta ttc cca aat tat gac aca cgc acg tac cca atg gaa acg aaa	768
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys	
245 250 255	
gca caa cta aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac	816
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn	
260 265 270	
gtg tct tca att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg	864
Val Ser Ser Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val	
275 280 285	

ata gaa tca tcc gtt att cga cca ccc cat gta ttt gat tat ata acg Ile Glu Ser Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr 290 295 300	912
gga ctc aca gtg tat aca caa tca aga agc att tct tcc gct cgc tat Gly Leu Thr Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr 305 310 315 320	960
ata aga cat tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg Ile Arg His Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg 325 330 335	1008
ggt agt aat ctt caa caa atg tat gga act aat caa aat cta cac agc Gly Ser Asn Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser 340 345 350	1056
act agt acc ttt gat ttt acg aat tat gat att tac aag act cta tca Thr Ser Thr Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser 355 360 365	1104
aag gat gca gta ctc ctt gat att gtt tac cct ggt tat acg tat ata Lys Asp Ala Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile 370 375 380	1152
ttt ttt gga atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat Phe Phe Gly Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn 385 390 395 400	1200
aat acc aga aag acg tta aag tat aat cca gtt tcc aaa gat att ata Asn Thr Arg Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile 405 410 415	1248
gcg agt aca aga gat tcg gaa tta gaa tta cct cca gaa act tca gat Ala Ser Thr Arg Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp 420 425 430	1296
caa cca aat tat gag tca tat agc cat aga tta tgt cat atc aca agt Gln Pro Asn Tyr Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser 435 440 445	1344
att ccc gcg acg ggt aac act acc gga tta gta cct gta ttt tct tgg Ile Pro Ala Thr Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp 450 455 460	1392
aca cat cga agt gca gat tta aac aat aca ata tat tca gat aaa atc Thr His Arg Ser Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile 465 470 475 480	1440
act caa att ccg gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca Thr Gln Ile Pro Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro 485 490 495	1488
gtg gta aaa gga cca gga cat aca gga ggg gat tta tta cag tat aat Val Val Lys Gly Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn 500 505 510	1536
aga agt act ggt tct gta gga acc tta ttt cta gct cga tat ggc cta Arg Ser Thr Gly Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu 515 520 525	1584
gca tta gaa aaa gca ggg aaa tat cgt gta aga ctg aga tat gct act Ala Leu Glu Lys Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr 1632	

530	535	540	
gat gca gat att gta ttg cat gta aac gat gct cag att cag atg cca			1680
Asp Ala Asp Ile Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro			
545	550	555	560
aaa aca atg aac cca ggt gag gat ctg aca tct aaa act ttt aaa gtt			1728
Lys Thr Met Asn Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val			
	565	570	575
gca gat gct atc aca aca tta aat tta gca aca gat agt tcg cta gca			1776
Ala Asp Ala Ile Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala			
	580	585	590
ttg aaa cat aat tta ggt gaa gac cct aat tca aca tta tct ggt ata			1824
Leu Lys His Asn Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile			
	595	600	605
gtt tac gtt gac cga atc gaa ttc atc cca gta gat taa			1863
Val Tyr Val Asp Arg Ile Glu Phe Ile Pro Val Asp *			
610	615	620	
<210> 42			
<211> 620			
<212> PRT			
<213> Bacillus thuringiensis (mutated)			
<400> 42			
Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu			
1	5	10	15
Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys			
	20	25	30
Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu			
	35	40	45
Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln			
	50	55	60
Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile			
	65	70	75
Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly			
	85	90	95
Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn			
	100	105	110
Pro Leu Arg Met Ser Asn Gly Ser Arg Ala Leu Arg Asp Val Arg Asn			
	115	120	125
Arg Phe Glu Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe			
	130	135	140
Arg Val Thr Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala			
	145	150	155
Ala Asn Leu His Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu			
	165	170	175
Glu Trp Gly Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln			
	180	185	190
Met Lys Leu Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu			
	195	200	205
Thr Gly Leu Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp			
	210	215	220
Tyr Asn Gln Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val			
	225	230	235
Ala Leu Phe Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys			
	245	250	255
Ala Gln Leu Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn			
	260	265	270



tct act tct gta tcc aat gat tct aac aga tac cct ttt gcg aat gag	96
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
cca aca aat gcg cta caa aat atg gat tat aaa gat tat tta aaa atg	144
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt gtt	192
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa tta	240
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt tat	288
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa tgg	336
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata gca	384
Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	
gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt aat	432
Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly Asn	
130 135 140	
aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat cca	480
Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn Pro	
145 150 155 160	
tta aga atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa atc	528
Leu Arg Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu Ile	
165 170 175	
ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca aat	576
Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr Asn	
180 185 190	
ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt cat	624
Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu His	
195 200 205	
tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga tgg	672
Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly Trp	
210 215 220	
tca aca act act att aat aac tat tat gat cgt caa atg aaa ctt act	720
Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu Thr	
225 230 235 240	
gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta gca	768
Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu Ala	
245 250 255	
aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa ttc	816
Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln Phe	

260	265	270	
cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc cca			864
Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe Pro			
275	280	285	
aat tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta aca			912
Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu Thr			
290	295	300	
agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca att			960
Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser Ile			
305	310	315	320
ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca tcc			1008
Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser Ser			
325	330	335	
gtt att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca gtg			1056
Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr Val			
340	345	350	
tat aca caa tca aga agc att tct tcc gct cgc tat ata aga cat tgg			1104
Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His Trp			
355	360	365	
gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt aat ctt			1152
Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn Leu			
370	375	380	
caa caa atg tat gga act aat caa aat cta cac agc act agt acc ttt			1200
Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr Phe			
385	390	395	400
gat ttt acg aat tat gat att tac aag act cta tca aag gat gca gta			1248
Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala Val			
405	410	415	
ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga atg			1296
Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly Met			
420	425	430	
cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga aag			1344
Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg Lys			
435	440	445	
acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca aga			1392
Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr Arg			
450	455	460	
gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat tat			1440
Asp Ser Glu Leu Glu Leu Pro Pro Glu Thr Ser Asp Gln Pro Asn Tyr			
465	470	475	480
gag tca tat agc cat aga tta tgt cat atc aca agt att ccc gcg acg			1488
Glu Ser Tyr Ser His Arg Leu Cys His Ile Thr Ser Ile Pro Ala Thr			
485	490	495	
ggt aac act acc gga tta gta cct gta ttt tct tgg aca cat cga agt			1536
Gly Asn Thr Thr Gly Leu Val Pro Val Phe Ser Trp Thr His Arg Ser			
500	505	510	
gca gat tta aac aat aca ata tat tca gat aaa atc act caa att ccg			1584

Ala Asp Leu Asn Asn Thr Ile Tyr Ser Asp Lys Ile Thr Gln Ile Pro	
515 520 525	
gcc gtt aaa tgt tgg gat aat tta ccg ttt gtt cca gtg gta aaa gga	1632
Ala Val Lys Cys Trp Asp Asn Leu Pro Phe Val Pro Val Val Lys Gly	
530 535 540	
cca gga cat aca gga ggg gat tta tta cag tat aat aga agt act ggt	1680
Pro Gly His Thr Gly Gly Asp Leu Leu Gln Tyr Asn Arg Ser Thr Gly	
545 550 555 560	
tct gta gga acc tta ttt cta gct cga tat ggc cta gca tta gaa aaa	1728
Ser Val Gly Thr Leu Phe Leu Ala Arg Tyr Gly Leu Ala Leu Glu Lys	
565 570 575	
gca ggg aaa tat cgt gta aga ctg aga tat gct act gat gca gat att	1776
Ala Gly Lys Tyr Arg Val Arg Leu Arg Tyr Ala Thr Asp Ala Asp Ile	
580 585 590	
gta ttg cat gta aac gat gct cag att cag atg cca aaa aca atg aac	1824
Val Leu His Val Asn Asp Ala Gln Ile Gln Met Pro Lys Thr Met Asn	
595 600 605	
cca ggt gag gat ctg aca tct aaa act ttt aaa gtt gca gat gct atc	1872
Pro Gly Glu Asp Leu Thr Ser Lys Thr Phe Lys Val Ala Asp Ala Ile	
610 615 620	
aca aca tta aat tta gca aca gat agt tcg cta gca ttg aaa cat aat	1920
Thr Thr Leu Asn Leu Ala Thr Asp Ser Ser Leu Ala Leu Lys His Asn	
625 630 635 640	
tta ggt gaa gac cct aat tca aca tta tct ggt ata gtt tac gtt gac	1968
Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp	
645 650 655	
cga atc gaa ttc atc cca gta gat gag aca tat gaa gcg gaa taa	2013
Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu *	
660 665 670	

<210> 44  
 <211> 670  
 <212> PRT  
 <213> Bacillus thuringiensis (mutated)

<400> 44	
Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala Thr Pro	
1 5 10 15	
Ser Thr Ser Val Ser Asn Asp Ser Asn Arg Tyr Pro Phe Ala Asn Glu	
20 25 30	
Pro Thr Asn Ala Leu Gln Asn Met Asp Tyr Lys Asp Tyr Leu Lys Met	
35 40 45	
Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu Val	
50 55 60	
Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys Leu	
65 70 75 80	
Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu Tyr	
85 90 95	
Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln Trp	
100 105 110	
Glu Ile Phe Met Glu Gln Val Glu Leu Ile Asn Gln Lys Ile Ala	
115 120 125	





625                      630                      635                      640  
 Leu Gly Glu Asp Pro Asn Ser Thr Leu Ser Gly Ile Val Tyr Val Asp  
                          645                      650                      655  
 Arg Ile Glu Phe Ile Pro Val Asp Glu Thr Tyr Glu Ala Glu  
                          660                      665                      670

<210> 45  
 <211> 1854  
 <212> DNA  
 <213> *Bacillus thuringiensis* (mutated)

<220>  
 <221> CDS  
 <222> (1)...(1854)

<221> misc\_feature  
 <222> (0)...(0)  
 <223> LRMS.R49PVD

<400> 45  
 atg tct gcg gga aat gct agt gaa tac cct ggt tca cct gaa gta ctt 48  
 Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu  
   1                          5                          10                          15  
  
 gtt agc gga caa gat gca gct aag gcc gca att gat ata gta ggt aaa 96  
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ala Ile Asp Ile Val Gly Lys  
                           20                          25                          30  
  
 tta cta tca ggt tta ggg gtc cca ttt gtt ggg ccg ata gtg agt ctt 144  
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu  
                           35                          40                          45  
  
 tat act caa ctt att gat att ctg tgg cct tca ggg gaa aag agt caa 192  
 Tyr Thr Gln Leu Ile Asp Ile Leu Trp Pro Ser Gly Glu Lys Ser Gln  
                           50                          55                          60  
  
 tgg gaa att ttt atg gaa caa gta gaa gaa ctc att aat caa aaa ata 240  
 Trp Glu Ile Phe Met Glu Gln Val Glu Glu Leu Ile Asn Gln Lys Ile  
   65                          70                          75                          80  
  
 gca gaa tat gca agg aat aaa gcg ctt tcg gaa tta gaa gga tta ggt 288  
 Ala Glu Tyr Ala Arg Asn Lys Ala Leu Ser Glu Leu Glu Gly Leu Gly  
                           85                          90                          95  
  
 aat aat tac caa tta tat cta act gcg ctt gaa gaa tgg gaa gaa aat 336  
 Asn Asn Tyr Gln Leu Tyr Leu Thr Ala Leu Glu Glu Trp Glu Glu Asn  
                           100                          105                          110  
  
 cca tta aga atg tct aga gcc tta cga gat gtg cga aat cga ttt gaa 384  
 Pro Leu Arg Met Ser Arg Ala Leu Arg Asp Val Arg Asn Arg Phe Glu  
                           115                          120                          125  
  
 atc ctg gat agt tta ttt acg caa tat atg cca tct ttt aga gtg aca 432  
 Ile Leu Asp Ser Leu Phe Thr Gln Tyr Met Pro Ser Phe Arg Val Thr  
                           130                          135                          140  
  
 aat ttt gaa gta cca ttc ctt act gta tat gca atg gca gcc aac ctt 480  
 Asn Phe Glu Val Pro Phe Leu Thr Val Tyr Ala Met Ala Ala Asn Leu  
   145                          150                          155                          160  
  
 cat tta ctg tta tta aag gac gcg tca att ttt gga gaa gaa tgg gga 528  
 His Leu Leu Leu Leu Lys Asp Ala Ser Ile Phe Gly Glu Glu Trp Gly

165	170	175	
tgg tca aca act act att aat aac tat tat gat cgt caa atg aaa ctt			576
Trp Ser Thr Thr Thr Ile Asn Asn Tyr Tyr Asp Arg Gln Met Lys Leu			
180	185	190	
act gca gaa tat tct gat cac tgt gta aag tgg tat gaa act ggt tta			624
Thr Ala Glu Tyr Ser Asp His Cys Val Lys Trp Tyr Glu Thr Gly Leu			
195	200	205	
gca aaa tta aaa ggc acg agc gct aaa caa tgg gtt gac tat aac caa			672
Ala Lys Leu Lys Gly Thr Ser Ala Lys Gln Trp Val Asp Tyr Asn Gln			
210	215	220	
ttc cgt aga gaa atg aca ctg gcg gtt tta gat gtt gtt gca tta ttc			720
Phe Arg Arg Glu Met Thr Leu Ala Val Leu Asp Val Val Ala Leu Phe			
225	230	235	240
cca aat tat gac aca cgc acg tac cca atg gaa acg aaa gca caa cta			768
Pro Asn Tyr Asp Thr Arg Thr Tyr Pro Met Glu Thr Lys Ala Gln Leu			
245	250	255	
aca agg gaa gta tat aca gat cca ctg ggc gcg gta aac gtg tct tca			816
Thr Arg Glu Val Tyr Thr Asp Pro Leu Gly Ala Val Asn Val Ser Ser			
260	265	270	
att ggt tcc tgg tat gac aaa gca cct tct ttc gga gtg ata gaa tca			864
Ile Gly Ser Trp Tyr Asp Lys Ala Pro Ser Phe Gly Val Ile Glu Ser			
275	280	285	
tcc gtt att cga cca ccc cat gta ttt gat tat ata acg gga ctc aca			912
Ser Val Ile Arg Pro Pro His Val Phe Asp Tyr Ile Thr Gly Leu Thr			
290	295	300	
gtg tat aca caa tca aga agc att tct tcc gct cgc tat ata aga cat			960
Val Tyr Thr Gln Ser Arg Ser Ile Ser Ser Ala Arg Tyr Ile Arg His			
305	310	315	320
tgg gct ggt cat caa ata agc tac cat cgt gtc agt agg ggt agt aat			1008
Trp Ala Gly His Gln Ile Ser Tyr His Arg Val Ser Arg Gly Ser Asn			
325	330	335	
ctt caa caa atg tat gga act aat caa aat cta cac agc act agt acc			1056
Leu Gln Gln Met Tyr Gly Thr Asn Gln Asn Leu His Ser Thr Ser Thr			
340	345	350	
ttt gat ttt acg aat tat gat att tac aag act cta tca aag gat gca			1104
Phe Asp Phe Thr Asn Tyr Asp Ile Tyr Lys Thr Leu Ser Lys Asp Ala			
355	360	365	
gta ctc ctt gat att gtt tac cct ggt tat acg tat ata ttt ttt gga			1152
Val Leu Leu Asp Ile Val Tyr Pro Gly Tyr Thr Tyr Ile Phe Phe Gly			
370	375	380	
atg cca gaa gtc gag ttt ttc atg gta aac caa ttg aat aat acc aga			1200
Met Pro Glu Val Glu Phe Phe Met Val Asn Gln Leu Asn Asn Thr Arg			
385	390	395	400
aag acg tta aag tat aat cca gtt tcc aaa gat att ata gcg agt aca			1248
Lys Thr Leu Lys Tyr Asn Pro Val Ser Lys Asp Ile Ile Ala Ser Thr			
405	410	415	
aga gat tcg gaa tta gaa tta cct cca gaa act tca gat caa cca aat			1296

Arg	Asp	Ser	Glu	Leu	Glu	Leu	Pro	Pro	Glu	Thr	Ser	Asp	Gln	Pro	Asn		
			420					425					430				
tat	gag	tca	tat	agc	cat	aga	tta	tgt	cat	atc	aca	agt	att	ccc	gcg	1344	
Tyr	Glu	Ser	Tyr	Ser	His	Arg	Leu	Cys	His	Ile	Thr	Ser	Ile	Pro	Ala		
			435				440					445					
acg	ggt	aac	act	acc	gga	tta	gta	cct	gta	ttt	tct	tg	aca	cat	cga	1392	
Thr	Gly	Asn	Thr	Thr	Gly	Leu	Val	Pro	Val	Phe	Ser	Trp	Thr	His	Arg		
			450			455					460						
agt	gca	gat	tta	aac	aat	aca	ata	tat	tca	gat	aaa	atc	act	caa	att	1440	
Ser	Ala	Asp	Leu	Asn	Asn	Thr	Ile	Tyr	Ser	Asp	Lys	Ile	Thr	Gln	Ile		
			465			470				475					480		
ccg	gcc	gtt	aaa	tgt	tg	gat	aat	tta	ccg	ttt	gtt	cca	gtg	gta	aaa	1488	
Pro	Ala	Val	Lys	Cys	Trp	Asp	Asn	Leu	Pro	Phe	Val	Pro	Val	Val	Lys		
				485					490						495		
gga	cca	gga	cat	aca	gga	ggg	gat	tta	tta	cag	tat	aat	aga	agt	act	1536	
Gly	Pro	Gly	His	Thr	Gly	Gly	Asp	Leu	Leu	Gln	Tyr	Asn	Arg	Ser	Thr		
			500				505						510				
ggt	tct	gta	gga	acc	tta	ttt	cta	gct	cga	tat	ggc	cta	gca	tta	gaa	1584	
Gly	Ser	Val	Gly	Thr	Leu	Phe	Leu	Ala	Arg	Tyr	Gly	Leu	Ala	Leu	Glu		
			515				520					525					
aaa	gca	ggg	aaa	tat	cgt	gta	aga	ctg	aga	tat	gct	act	gat	gca	gat	1632	
Lys	Ala	Gly	Lys	Tyr	Arg	Val	Arg	Leu	Arg	Tyr	Ala	Thr	Asp	Ala	Asp		
			530			535					540						
att	gta	ttg	cat	gta	aac	gat	gct	cag	att	cag	atg	cca	aaa	aca	atg	1680	
Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys	Thr	Met		
			545			550				555					560		
aac	cca	ggt	gag	gat	ctg	aca	tct	aaa	act	ttt	aaa	gtt	gca	gat	gct	1728	
Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala	Asp	Ala		
				565					570						575		
atc	aca	aca	tta	aat	tta	gca	aca	gat	agt	tcg	cta	gca	ttg	aaa	cat	1776	
Ile	Thr	Thr	Leu	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Leu	Ala	Leu	Lys	His		
			580					585						590			
aat	tta	ggt	gaa	gac	cct	aat	tca	aca	tta	tct	gg	ata	gtt	tac	gtt	1824	
Asn	Leu	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val	Tyr	Val		
			595				600					605					
gac	cga	atc	gaa	ttc	atc	cca	gta	gat	taa							1854	
Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp	*								
			610			615											

<210> 46  
 <211> 617  
 <212> PRT  
 <213> Bacillus thuringiensis (mutated)

<400> 46  
 Met Ser Ala Gly Asn Ala Ser Glu Tyr Pro Gly Ser Pro Glu Val Leu  
 1 5 10 15  
 Val Ser Gly Gln Asp Ala Ala Lys Ala Ile Asp Ile Val Gly Lys  
 20 25 30  
 Leu Leu Ser Gly Leu Gly Val Pro Phe Val Gly Pro Ile Val Ser Leu

		35					40					45				
Tyr	Thr	Gln	Leu	Ile	Asp	Ile	Leu	Trp	Pro	Ser	Gly	Glu	Lys	Ser	Gln	
	50					55					60					
Trp	Glu	Ile	Phe	Met	Glu	Gln	Val	Glu	Glu	Leu	Ile	Asn	Gln	Lys	Ile	
65				70						75					80	
Ala	Glu	Tyr	Ala	Arg	Asn	Lys	Ala	Leu	Ser	Glu	Leu	Glu	Gly	Leu	Gly	
				85					90					95		
Asn	Asn	Tyr	Gln	Leu	Tyr	Leu	Thr	Ala	Leu	Glu	Glu	Trp	Glu	Glu	Asn	
			100					105					110			
Pro	Leu	Arg	Met	Ser	Arg	Ala	Leu	Arg	Asp	Val	Arg	Asn	Arg	Phe	Glu	
		115				120					125					
Ile	Leu	Asp	Ser	Leu	Phe	Thr	Gln	Tyr	Met	Pro	Ser	Phe	Arg	Val	Thr	
	130					135					140					
Asn	Phe	Glu	Val	Pro	Phe	Leu	Thr	Val	Tyr	Ala	Met	Ala	Ala	Asn	Leu	
145					150					155					160	
His	Leu	Leu	Leu	Leu	Lys	Asp	Ala	Ser	Ile	Phe	Gly	Glu	Glu	Trp	Gly	
				165					170					175		
Trp	Ser	Thr	Thr	Thr	Ile	Asn	Asn	Tyr	Tyr	Asp	Arg	Gln	Met	Lys	Leu	
			180					185					190			
Thr	Ala	Glu	Tyr	Ser	Asp	His	Cys	Val	Lys	Trp	Tyr	Glu	Thr	Gly	Leu	
	195					200						205				
Ala	Lys	Leu	Lys	Gly	Thr	Ser	Ala	Lys	Gln	Trp	Val	Asp	Tyr	Asn	Gln	
	210					215					220					
Phe	Arg	Arg	Glu	Met	Thr	Leu	Ala	Val	Leu	Asp	Val	Val	Ala	Leu	Phe	
225					230					235					240	
Pro	Asn	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Met	Glu	Thr	Lys	Ala	Gln	Leu	
			245					250					255			
Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Gly	Ala	Val	Asn	Val	Ser	Ser	
			260					265				270				
Ile	Gly	Ser	Trp	Tyr	Asp	Lys	Ala	Pro	Ser	Phe	Gly	Val	Ile	Glu	Ser	
	275					280					285					
Ser	Val	Ile	Arg	Pro	Pro	His	Val	Phe	Asp	Tyr	Ile	Thr	Gly	Leu	Thr	
	290					295					300					
Val	Tyr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Ser	Ala	Arg	Tyr	Ile	Arg	His	
305				310						315					320	
Trp	Ala	Gly	His	Gln	Ile	Ser	Tyr	His	Arg	Val	Ser	Arg	Gly	Ser	Asn	
			325					330					335			
Leu	Gln	Gln	Met	Tyr	Gly	Thr	Asn	Gln	Asn	Leu	His	Ser	Thr	Ser	Thr	
			340					345				350				
Phe	Asp	Phe	Thr	Asn	Tyr	Asp	Ile	Tyr	Lys	Thr	Leu	Ser	Lys	Asp	Ala	
	355					360					365					
Val	Leu	Leu	Asp	Ile	Val	Tyr	Pro	Gly	Tyr	Thr	Tyr	Ile	Phe	Phe	Gly	
	370				375						380					
Met	Pro	Glu	Val	Glu	Phe	Phe	Met	Val	Asn	Gln	Leu	Asn	Asn	Thr	Arg	
385					390					395						

Ile	Val	Leu	His	Val	Asn	Asp	Ala	Gln	Ile	Gln	Met	Pro	Lys	Thr	Met
545					550					555					560
Asn	Pro	Gly	Glu	Asp	Leu	Thr	Ser	Lys	Thr	Phe	Lys	Val	Ala	Asp	Ala
				565					570						575
Ile	Thr	Thr	Leu	Asn	Leu	Ala	Thr	Asp	Ser	Ser	Leu	Ala	Leu	Lys	His
			580					585					590		
Asn	Leu	Gly	Glu	Asp	Pro	Asn	Ser	Thr	Leu	Ser	Gly	Ile	Val	Tyr	Val
		595					600					605			
Asp	Arg	Ile	Glu	Phe	Ile	Pro	Val	Asp							
	610					615									

<210> 47  
 <211> 12  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> LRMS Insert

<400> 47  
 ttaagaatgt ct

12

<210> 48  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> LRMS Insert

<400> 48  
 Leu Arg Met Ser  
 1